

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:05:54 ; Search time 13.54 Seconds

(without alignments)
1286.839 Million cell updates/sec

Title: US-09-471-459A-5

Perfect score: 2408

Sequence: 1 MSLMVERCGEILFENPDQN.....PDHDAAGGTSESEQEGDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	100.0	450	1 CN7B_HUMAN	09np56 homo sapien
2	2192	91.0	446	1 CN7B_MOUSE	09q9x1 mus musculu
3	1425.5	59.2	456	1 CN7A_MOUSE	P70453 mus musculu
4	1419.5	58.9	482	1 CN7A_HUMAN	Q13346 homo sapien
5	1397.5	58.0	426	1 CN7A_RAT	008593 rattus norv
6	604.5	25.1	809	1 CN4D_HUMAN	008499 homo sapien
7	603.5	25.1	672	1 CN4D_RAT	P14270 rattus norv
8	580.5	24.1	721	1 CN4B_RAT	P14646 rattus norv
9	567.5	23.6	736	1 CN4B_HUMAN	Q07343 homo sapien
10	565	23.5	886	1 CN4A_HUMAN	P27815 homo sapien
11	559.5	23.2	610	1 CN4Z_RAT	P14645 rattus norv
12	559.5	23.2	844	1 CN4A_RAT	P54748 rattus norv
13	553	23.0	712	1 CN4C_HUMAN	008493 homo sapien
14	529.5	22.0	536	1 CN4C_RAT	P14644 rattus norv
15	517	21.5	549	1 Y571_CAEEL	Q22000 caenorhabd
16	493	20.5	584	1 CN4I_DROME	P12352 drosophil
17	468	19.4	535	1 CN1B_MOUSE	001065 mus musculu
18	467	19.4	534	1 CN1B_BOVIN	001061 bos taurus
19	466	19.4	534	1 CN1A_HUMAN	P54750 homo sapien
20	466	19.4	535	1 CN1B_RAT	001066 rattus norv
21	466	19.4	565	1 CN1A_MOUSE	061481 mus musculu
22	461	19.1	664	1 YFGK_CAEEL	Q18696 caenorhabd
23	461	19.1	793	1 REGA_DICDI	Q23917 dictyostell
24	460	19.1	823	1 CN8A_MOUSE	088502 mus musculu
25	454.5	18.9	529	1 CN1A_BOVIN	P14100 bos taurus
26	452.5	18.8	768	1 CN1C_RAT	Q63421 rattus norv
27	450.5	18.7	654	1 CN1C_MOUSE	Q64338 mus musculu
28	449	18.6	536	1 CN1B_HUMAN	001064 homo sapien
29	448.5	18.6	709	1 CN1C_HUMAN	Q14123 homo sapien
30	445.5	18.5	713	1 CN8B_HUMAN	060658 homo sapien
31	441	18.3	659	1 CN8B_HUMAN	095263 homo sapien
32	422	17.5	534	1 CN9A_MOUSE	070628 mus musculu
33	399	16.6	593	1 CN9A_HUMAN	076083 homo sapien

34	381	15.8	875	1 CN5A_HUMAN	076074 homo sapien
35	378	15.7	865	1 CN5A_CANFA	077746 canis fami1
36	375	15.6	865	1 CN5B_BOVIN	Q28156 bos taurus
37	368.5	15.3	1112	1 CN5B_HUMAN	Q13370 homo sapien
38	362	15.0	833	1 CN5A_RAT	054735 rattus norv
39	357.5	14.8	1108	1 CN3B_RAT	063085 rattus norv
40	354	14.7	799	1 CN3B_MOUSE	061409 mus musculu
41	351	14.6	1141	1 CN3A_RAT	062865 rattus norv
42	346	14.4	1141	1 CN3A_HUMAN	Q14432 homo sapien
43	303.5	12.6	858	1 CN8C_HUMAN	P51160 homo sapien
44	300	12.5	855	1 CN8C_BOVIN	P16586 bos taurus
45	299	12.4	928	1 CN2A_RAT	Q01062 rattus norv

ALIGNMENTS

RESULT 1
ID CN7B_HUMAN STANDARD: PRT; 450 AA.
AC 09np56:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=20275458; PubMed=10814504;
RX Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC INSENSITIVE TO ZAPRINAST, ROTIPRAM, AND MILRINONE.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN
CC HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL: AB038040; BAA96537.1; -
CC DR EMBL: AJ251860; CAB92441.1; -
CC DR MIM: 604645; -
CC DR InterPro: IPR003607; HDC.
CC DR InterPro: IPR002073; PDEase.
CC DR

DR Pfam: PF00233; PDEase: 1.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00471; Hdc: 1.
 DR PROSITE: PS00126; PDEASE_I; 1.
 KW Hydrolase: CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 100.0%; Score 2408; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 9.6e-188;
 Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSCLMVERGCEILFENPDONAKVCMLGDIRLKGOTGVAERGRSGYPFIDFRLNSTTYS 60
 1 MSLCMVERGCEILFENPDONAKVCMLGDIRLKGOTGVAERGRSGYPFIDFRLNSTTYS 60
 61 GEIGTKKKVKRLSFOYRFHNSRLRGIIIPQAPLHLLDEDDYLGOARHMLSKYGMDDPDI 120
 61 GEIGTKKKVKRLSFOYRFHNSRLRGIIIPQAPLHLLDEDDYLGOARHMLSKYGMDDPDI 120
 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKIDMTYTLRFLVYQEDYHSQNPYHNAVHAAD 180
 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKIDMTYTLRFLVYQEDYHSQNPYHNAVHAAD 180
 181 VTOAMHCYKLEPKLASFLTPDLIMGLLAAAHVDHPGVNOPELKTNNHLANLYONMS 240
 181 VTOAMHCYKLEPKLASFLTPDLIMGLLAAAHVDHPGVNOPELKTNNHLANLYONMS 240
 241 VLENHNRSTIGMLRESRLAHLPRKEMTODIEQOLGSLIATDINRONEFLTRKAKHLN 300
 241 VLENHNRSTIGMLRESRLAHLPRKEMTODIEQOLGSLIATDINRONEFLTRKAKHLN 300
 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSEBVEEYFROGELEBOKKELEIS 360
 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSEBVEEYFROGELEBOKKELEIS 360
 361 PLCNQOKDSIPSIQIGFMSYIVELPRFMAHFTGNSTLENNMLGHANNAKQMSLLRPQ 420
 361 PLCNQOKDSIPSIQIGFMSYIVELPRFMAHFTGNSTLENNMLGHANNAKQMSLLRPQ 420
 421 HRSRGSSGSDPDHDAOGTSESEDEGSDSP 450
 421 HRSRGSSGSDPDHDAOGTSESEDEGSDSP 450

RESULT 2
 CN7B_MOUSE STANDARD: PRT: 446 AA.
 AC 030XOL;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE cAMP-specific 3',5'-cyclic phosphodiesterase 7B (BC 3.1.4.17).
 GN PDE7B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087273; PubMed=10618442;
 RA Hatanu J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
 RT "Cloning and characterization of PDE7B, a cAMP-specific
 RT Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C7BL/6J;
 RX MEDLINE=20329226; PubMed=10872825;
 RA Gardner C.E., Robas N.M., Gawkill D., Fidoock M.D.;
 RT "Cloning and characterisation of the human and mouse PDE7B, a novel
 RT cAMP-specific nucleotide phosphodiesterase.";

RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
 CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
 CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 CC ADENOSINE 5'-PHOSPHATE.
 CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
 CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
 CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
 CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
 CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
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 CC -----
 DR EMBL: AF190638; AAF25195.1; -
 DR EMBL: AJ251859; CAB92530.1; -
 DR MGD: MGI:1352752; Pde7b.
 DR InterPro: IPR003607; Hdc.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00471; Hdc; 1.
 DR PROSITE: PS00126; PDEASE_I; 1.
 KW Hydrolase: CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 446 AA; 51337 MW; 7C052664B593A5A8 CRC64;

Query Match 91.0%; Score 2192; DB 1; Length 446;
 Best Local Similarity 91.6%; Pred. No. 3e-170;
 Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

1 MSCLMVERGCEILFENPDONAKVCMLGDIRLKGOTGVAERGRSGYPFIDFRLNSTTYS 60
 1 MSLCMVERGCEILFENPDONAKVCMLGDIRLKGOTGVAERGRSGYPFIDFRLNSTTYS 60
 61 GEIGTKKKVKRLSFOYRFHNSRLRGIIIPQAPLHLLDEDDYLGOARHMLSKYGMDDPDI 120
 61 GEIGTKKKVKRLSFOYRFHNSRLRGIIIPQAPLHLLDEDDYLGOARHMLSKYGMDDPDI 120
 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKIDMTYTLRFLVYQEDYHSQNPYHNAVHAAD 180
 121 LFDRLTNGNSLVTLCHLFTNTHGLIHFKIDMTYTLRFLVYQEDYHSQNPYHNAVHAAD 180
 181 VTOAMHCYKLEPKLASFLTPDLIMGLLAAAHVDHPGVNOPELKTNNHLANLYONMS 240
 181 VTOAMHCYKLEPKLASFLTPDLIMGLLAAAHVDHPGVNOPELKTNNHLANLYONMS 240
 181 VTOAMHCYKLEPKLASFLTPDLIMGLLAAAHVDHPGVNOPELKTNNHLANLYONMS 240
 241 VLENHNRSTIGMLRESRLAHLPRKEMTODIEQOLGSLIATDINRONEFLTRKAKHLN 300
 241 VLENHNRSTIGMLRESRLAHLPRKEMTODIEQOLGSLIATDINRONEFLTRKAKHLN 300
 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSEBVEEYFROGELEBOKKELEIS 360
 301 KDLRLDADDRHFMQIALKCADICNPCRIMWMSKOMSEBVEEYFROGELEBOKKELEIS 360
 361 PLCNQOKDSIPSIQIGFMSYIVELPRFMAHFTGNSTLENNMLGHANNAKQMSLLRPQ 420
 361 PLCNQOKDSIPSIQIGFMSYIVELPRFMAHFTGNSTLENNMLGHANNAKQMSLLRPQ 420
 421 HRSRGSSGSDPDHDAOGTSESEDEGSDSP 450
 421 HRSRGSSGSDPDHDAOGTSESEDEGSDSP 450
 421 HRSRGSSGSDPDHDAOGTSESEDEGSDSP 450

Oy	127	NGNSLVTLCHLENTFHCILHFKLMDWTYLRFLVMQVEDHYHSQNRYHNAAVADYTQAMH	186
Db	140	NGNSLVLTFLFELSHLCHELFPHLDWKKRFLVMJQEEDYHSQNPYHNAAVADYTQAMH	199
Oy	187	CYLEKPKIASFLPLDLMELLLAAAHADVPCVNOPFLIKTNHHLANLYOMSYLENHH	246
Db	200	CYLEKPKLASVTPMWDLLSLIAAATHDDHPGVNOPEFLIKTNHHIATLYTKSSVYLENNH	259
Oy	247	WRSTIGMLRESRLHLAKPMKTODIDEOGSLIATDINKONEPFLTRKLANKDLKYLE	306
Db	260	WRSVAGLGRLREGSFLSHLPESROEMEAQIGALLIATDISRONEXYSLFSHDKDDLHD	319
Oy	307	DAORHMLIOALKAICAIQCPRTIMWSKMSRVCEEFYRGCELFOKEPLEISPLCQQ	366
Db	320	DGRHRHLVLQALKCAIQICPCRKMWELSKMSSEKYTEEFFHGDDLEKKHGLVSPLCDRQ	379
Oy	367	KDSIPSIQIGMSYVEPLREVAHFHTGNSTSENMLGIHLNKAQWKSLPLPRQRSBGS	426
Db	380	TESTANIQIGMTYLVEPLTFEVARRSA-TRLSQTMLGHVGLNKASWKQLQGQSSSDA	438
Oy	427	SGS 429	
Db	439	NAA 441	
RESULT	4		
ID	CNTA_HUMAN	STANDARD;	PRT; 482 AA.
AC	O13946; O15380;		
DT	15-JUL-1998 (Rel. 36, Created)		
DR	15-JUL-1998 (Rel. 36, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A (EC 3.1.4.11) (HCP1) (TM22).		
GN	PDE7A.		
OC	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (PDE7A1).		
RX	MEDLINE=93286141; PubMed=8369765;		
RA	Michael T., Bloom T.J., Martins R., Loughney K., Ferguson K., Riggs M., Rodgers L., Beavo J.A., Wigler M.;		
RT	"Isolation and characterization of a previously undetected human cAMP phosphodiesterase by complementation of cAMP phosphodiesterase-		
RL	deficient Saccharomyces cerevisiae." ; J. Biol. Chem. 268:12925-12932(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A. (PDE7A2).		
RC	TISSUE=skeletal muscle;		
RX	MEDLINE=97341143; PubMed=9195912;		
RA	Han P., Zhu X., Michael T.;		
RT	"Alternative splicing of the high affinity cAMP-specific phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart." ; J. Biol. Chem. 272:16152-16157(1997).		
RL	J. Biol. Chem. 272:16152-16157(1997).		
CC	-I- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS PHOSPHODIESTERASE IS HIGHLY SPECIFIC FOR CAMP AND MAY HAVE A ROLE IN MUSCLE SIGNAL TRANSDUCTION.		
CC	-I- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2O) = ADENOSINE 5'-PHOSPHATE.		
CC	-I- COFACTOR: REQUIRES DIVALENT CATIONS.		
CC	-I- ENZYME REGULATION: INSENSITIVE TO ALL SELECTIVE PDE INHIBITORS.		
CC	-I- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.		
CC	-I- SUBCELLULAR LOCATION: PDE7A1 (57 kDa) IS LOCATED MOSTLY TO SOLUBLE CELLULAR FRACTIONS. PDE7A2 (50 kDa) IS LOCATED TO PARTICULATE CELLULAR FRACTIONS.		
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: PDE7A1 (SHOWN HERE) AND PDE7A2; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER AT THEIR N- TERMINAL REGION.		
CC	-I- TISSUE SPECIFICITY: PDE7A1 IS FOUND AT HIGH LEVELS IN SKELETAL		


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Db 218 KEKKRPMQISGVYKILMHSSSLNSCIPRGVKTEDVDLAKE---LEDVKNKGLHVF 274
QY 122 FDRLLNGSLVTLCH-LFNTHGLIHFKLMDLHRLVAVQEDYHSQNPYHNAVHAD 180
Db 275 IAEI-SGNRPILYIMHTFOERDLTKFKIPVDLTLYLMLTEHDVAVYHNHIAAD 333
QY 181 VTQAMHCYKPKLASFLTPDIMGLAAAHVDHGVNQPFLIKTNHNLANYOMNS 240
Db 334 VVQSTHVLSTPALLEAVTDEILAAITASAIHDVDHGVSNQPLINTSELALMYNDS 393
QY 241 VLENHMHSTIGMLRESR-LLAHLPEKMTODIEQGLSLIADINRONEFLRLKAHL 298
Db 394 VLENHHLAVGFKLLOEENCDFQMLTKQROSLRKMADIYLAIDMSKHMMLADLKTMY 453
QY 299 HNKD-----LRDADDRHMLDIALKADICNCPRIKRWMSKQSEVCEPFRQGLE 352
Db 454 ETKKVTSSGVLLLDNYSRIQVLONMVHCADLSNPKLOLYRQWTRIMEEFPQGDRE 513
QY 353 QKFELEISPLCNOQKDSIPSIQIFMSYIEPLFRENHAFNGNSTLSNNMLGHLAHNKAQ 412
Db 514 RERGMETSPMDKHNASVSKSQVGFIDYIVHPLMETWADLVHPD--KODIIDTLEDNRW 571
QY 413 WKSLLPQHRSRGSSGSPDHDHAGQGTSE-----EQEGDS 449
Db 572 YQSTIPQ-----SPSPAPDDQEDGROQGTKEQFELTLEDGDS 610

RESULT 8
CNAB_RAT ID CNAB_RAT STANDARD; PRT; 721 AA.
AC P14646;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-dependent 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17) (PDE4B).
GN PDE4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A. (PDE4B3).
RA Huston E., Simon L., Annette R., Catterall C., Ross A.H., Steele M.R.,
RA Bolger G.B., Perry M., Owens R., Houslay M.D.,
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE OF 160-721 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-89264471; PubMed-2542941;
RA Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
RA Wigler M.;
RT "Isolation and characterization of a mammalian gene encoding a high-
RT affinity CAMP phosphodiesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
RN 131
RP SEQUENCE OF 289-638 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-89315790; PubMed-2546153;
RA Swinnen J.V., Joseph D.R., Conli M.;
RT "Molecular cloning of rat homologues of the Drosophila melanogaster
RT dunce CAMP phosphodiesterase: evidence for a family of genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
RN 141
RP SEQUENCE FROM N.A. (PDE4B2).
RX MEDLINE-95047482; PubMed-7958996;
RA Bolger G.B., Rodgers L., Riggs M.;
RT "Differential CNS expression of alternative mRNA isoforms of the
RT mammalian genes encoding CAMP-specific phosphodiesterases.";
RL Gene 149:237-244(1994).
RN 151
RP SEQUENCE FROM N.A. (PDE4B2).

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RC STRAIN=WISTAR;
RX MEDLINE-94103234; PubMed-8276818;
RA Monaco L., Vicini E., Conli M.;
RT "Structure of two rat genes coding for closely related rolipram-
RT sensitive CAMP phosphodiesterases. Multiple mRNA variants originate
RT from alternative splicing and multiple stat sites.";
RL J. Biol. Chem. 269:347-357(1994).
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; PDE4B1, PDE4B2 AND
CC PDE4B3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC -----
DR EMBL; U95748; AAB96560.1; -
DR EMBL; J04563; AAA66039.1; -
DR EMBL; M25350; AAAA1846.1; -
DR EMBL; M28413; AAAA1824.1; -
DR EMBL; L27058; AAA74478.1; -
DR EMBL; U01291; AAA18926.1; -
DR EMBL; U01289; AAA18926.1; JOINED.
DR EMBL; U01293; AAA18926.1; JOINED.
DR EMBL; U01294; AAA18926.1; JOINED.
DR EMBL; U01295; AAA18926.1; JOINED.
DR EMBL; U01296; AAA18926.1; JOINED.
DR EMBL; U01297; AAA18926.1; JOINED.
DR EMBL; U01298; AAA18926.1; JOINED.
DR EMBL; U01290; AAA18926.1; JOINED.
DR PIR; D33904; D33904.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolyase; CAMP; Alternative splicing; Multigene family.
FT VARSPPLIC 1 196
FT MTAKNSKELEPASESEVCITFKQMRLELEPKLPGRPT
FT SPKISPRSPNSPCFPKRLVYNSIRRRFTVAHCFDY
FT ENGSPGRSPPLDQASSSGVLVLAAPFGHSGRSESLYRS
FT DSDYDLSPKAMSRNSLPSBOGDLDLVTPFAQVLAASRIY
FT RNNFTLTNLHGAPNKRSPASASQAPVTRVLSIO -> MKEGG
FT GTVGAGASSRGGGDSMAASIQPLPNTLSCLFA (IN
FT ISOFORM PDE4B2).
FT T -> S (IN REF. 5).
FT FT
FT SQ CONFLICT 516 516
FT SEQUENCE 721 AA; 82100 MW; C6FB885B6107BDAD CRC64;

Query Match 24.1%; Score 580.5; DB 1; Length 721;
Best Local Similarity 31.9%; Pred. No. 2.3e-39;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

QY 66 KKKYKRLS-----FQRYFNASRLGLIPQAPRLHLDDEDYLGQARHMLSKVGMDFDPL 121
Db 283 KKKKQQLMTQISGVYKILMHSSSLNNTSISRGVNTENDDLAKLEDLNK---WGLNIFN 339
QY 122 FDRLLNGSLVTLCH-LFNTHGLIHFKLMDLHRLVAVQEDYHSQNPYHNAVHAD 181
Db 340 VAGSHNRPILCYIMAITFOERDLTKFKISSDTFTVYMTLEDHYHSDVAVYHNHIAAD 399
QY 182 VTQAMHCYKPKLASFLTPDIMGLAAAHVDHGVNQPFLIKTNHNLANYOMNSV 241
Db 400 AOSTHVLSTPALDAVFTDEILAAITFAAAIHDVDHGVSNQPLINTSELALMYNDSV 459

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QY	242	LENNHNRSTGKALRER--LLAHLPKEMTIDEOGSLIATDINRQNEFLTRKAKHL	259
Db	460	LENNHNLAVGFKLLDGEHDDIFQNLTKRQKQRTIKRWIVLWATLADMSKHSLLADLKTYVE	519
QY	300	NKQ-----LRLEDADQHFMLQALAKCADCIDPCRIEMKMSQSPRCSEFQYGEQ	353
Db	520	TKKVTSSGVLLDNTDTRIOYLRNMYNCADLSNPYSLELYKQWMDRIEFPQDGKER	579
QY	354	KFELEISPLCNQXNSISISITIGMSATYVLEPRERAHHTGNSITSEWMLGHANRAQW	413
Db	580	ERCKEISPMCKHTKATSEKVSQVGFIDIVHPMETRADLVQDP--AQDILTLEDNRWY	637
QY	414	KSLILPR-----QHSKSGSGSGPNDH---ACQGISPEDEGDSF	450
Db	638	QSMIPQSPSPIDERSKDCQGLMEKTFQELTLEEDSEGPKEGDP	684
RESULT 9			
CC	CN4B_HUMAN	STANDARD:	PRT: 736 AA.
ID	Q07343.	015443.	
AC	01-FEB-1995	(Rel. 31, Created)	
DT	01-FEB-1995	(Rel. 31, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	cAMP-dependent 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)		
DE	(PDE4) (PDE32).		
GN	PDE4B.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RN	SEQUENCE FROM N.A. (PDE4B1 AND PDE4B2).		
RP	TISSUE=Brain;		
RC	MEDLINE=94019330; PubMed=8413254;		
RX	Bolger G., Michaeli T., Martins T., St John T., Steiner B.,		
RA	Rodgers L., Riggs M., Wiegler M., Ferguson K.;		
RT	"A family of human phosphodiesterases homologous to the dunce		
RT	learning and memory gene product of Drosophila melanogaster are		
RT	potential targets for antidepressant drugs.";		
RL	Mol. Cell. Biol. 13:6558-6571(1993).		
RL	[2]		
RP	SEQUENCE FROM N.A. (PDE4B3).		
RX	MEDLINE=98041898; PubMed=9371714;		
RA	Houston E., Lumb S., Russell A., Catterall C., Ross A.H., Steele M.R.,		
RA	Bolger G.B., Perry M.J., Owens R.J., Houslay M.D.,		
RT	"Molecular cloning and transient expression in COS7 cells of a novel		
RT	human PDE4B cAMP-specific phosphodiesterase, HSPDE4B3.";		
RL	Biochem. J. 328:549-558(1997).		
RN	[3]		
RN	SEQUENCE FROM N.A. (PDE4B2).		
RP	TISSUE=Brain;		
RC	MEDLINE=93203241; PubMed=8384210;		
RA	McLaughlin M.M., Cieslinski L.B., Burman M., Torphy T.J.,		
RA	Livi G.P.;		
RT	"A low Km, rolipram-sensitive, cAMP-specific phosphodiesterase from		
RT	human brain. Cloning and expression of cDNA, biochemical		
RT	characterization of recombinant protein, and tissue distribution of		
RT	mRNA.";		
RL	J. Biol. Chem. 268:6470-6476(1993).		
CC	-1- FUNCTION: MAY BE INVOLVED IN MEDIATING CENTRAL NERVOUS SYSTEM		
CC	EFFECTS OF THERAPEUTIC AGENTS RANGING FROM ANTIDEPRESSANTS TO		
CC	ANTASTHATIC AND ANTI-INFLAMMATORY AGENTS.		
CC	-1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =		
CC	ADENOSINE 5'-PHOSPHATE.		
CC	-1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.		
CC	-1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.		
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: PDE4B1 (SHOWN HERE),		
CC	PDE4B2 AND PDE4B3. ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, LUNG AND SKELETAL		
CC	MUSCLE.		
CC	-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE		
CC	FAMILY.		

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CC
DR EMBL; L20966; AAA03589.1; -
DR EMBL; L20971; AAA03593.1; -
DR EMBL; M97515; AAA06426.1; -
DR EMBL; U85046; AAB96381.1; -
DR MIM; 600127; -
DR InterPro; IPRO03607; HDC;
DR InterPro; IPRO02073; PDEase.
DR Pfam; PF00233; Pdease; 1.
DR PRINTS; PRO0387; PDLESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_1; 1.
DR Hydrobase; CAMP; Alternative splicing: Multigene family.
FT VARSPLIC 1 93 MKRSRVTWADNVNDYDECSLSKSYSSSSNTGIDLMR
FT FT GRRCSGNLOLPISOROSRRARTPEGDISPTPLPRTL
FT FT PSIAITTVSOE -> MYAKDSKEIYASPEVCITPFKEOM
FT FT HLEILPRLPBNRTSPKISPSRNPSNCFPKLLVKSI
FT FT KRRRFVAVHT (IN ISOFORM PDEA43) .
FT FT MKRSRVTWADNVNDYDECSLSKSYSSSSNTGIDLMR
FT FT GRRCSGNLOLPISOROSRRARTPEGDISPTPLPRTL
FT FT PSIAITTVSOCEPVENGSPGRSLPDPAASSACLVAT
FT FT PGHROSRESELYKSDDYDLSFKAMSRSLSPSHODDL
FT FT IVTFPAQVLASLRKRNNFPILTNLGTNKRGSPAASPPV
FT FT SRVNPQ -> MKRHGCTGFSTGISGSDSSMSDIAPLOP
FT FT NYMPVCLFA (IN ISOFORM PDEAB2).
SQ SEQUENCE 736 AA; 83343 MW; 208FC9CD40EF5B CRC64;
Query Match 23.6%; Score 567.5; DB: 1 Length 736;
Best Local Similarity 31.3%; Pred. No. 2,7e-38;
Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;
OY 66 KKKYKRLS----FOKYFHASRLAGIIPOARHLDEDYLGQAHHLSYGMMDIPTL 121
||| :||: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 298 KKKKOOLMTDISGVKKLHMSSSLNNTSISRGVTENEDHLAKLEDLNK--WGINTFN 354
OY 122 FDLRLTNGNSLVTLCHLFNFTHGLIHFFKLDMYTLRLRYVOEDYHSQNPNYAAYADY 181
DB 355 VAGYSNRHPFLTCIMAYIFOEKDLTKTERISSDTFTTMTELDYHSDVAYNHSLAAVD 414
OY 182 TQAHNCYLKEPKLASFLPLDIMLGLAAAHADVDFGVNOPLIKTNHHLANTYONNSV 241
DB 415 AQSHVYLSPALDAVFDTLETILAIFAALAIHDVDHGVSNOPLINTNSLAIVDESIV 474
OY 242 LENHNHSTIGMLRESR--LNAHLRKEMTODIEQLSLIADINDINFETLRILKAHLH 299
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 475 LENHHLAVGEKLLQEHCHDIFNNLKQRQTLRRKVINDVLAIDMSKHSMLADIATWE 534
OY 300 NKD-----LRLEDAADRHFMLQILKCAADCICNPCRIWESMKOWSERVACEEFGQEL 353
||| :||: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 535 TKKVTSGVLLDNTRYDIRIQVLRNWHCADLSNPTKSLLEYLRQTWDIREMEEFPOQGDKER 594
OY 354 KFELIELPICNOOKDIPISIOIGFSYIVEPYFERMAHFGNSNLSNMGIHLANHAKWM 413
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 595 ERGWETSIPMODKHKTASVEKSYGFIIDYIVHFLMETWADLVQRP--AQDILDIEDNRMY 652
OY 414 KSLLPRHRBSRSSGSGP---DHNHAC-----OGSESPEEGD 448
||| :||: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 653 QSMTPQ-----SPSPRLDEGNRCQGLMKRPFELTLDEBDSEGEPEKGE 697
RESULT 10
CN4A_HUMAN STANDARD. PROT. 886 AA.
ID CN4A_HUMAN
DC P27815; Q16253; O75522; O76092;
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DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE cAMP-dependent 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17)
 DE (PDE2) (PDE46).
 DE PDE4A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94019330; Pubmed=8413254;
 RA Bolger G., Michael T., Martins T., St John T., Steiner B.,
 RA Rodgers L., Riggs M., Wiegler M., Ferguson K.,
 RT "A family of human phosphodiesterases homologous to the dunce
 RT learning and memory gene product of *Drosophila melanogaster* are
 RT potential targets for antidepressant drugs.";
 RL Mol. Cell. Biol. 13:6558-6571(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (PDE4A RD1).
 RX TISSUE=Brain;
 RX MEDLINE=96343959; Pubmed=9677330.
 RA Sullivan M., Rena G., Beggs F., Gordon L., Olsen A.S., Houslay M.D.,
 RT "Identification and characterization of the human homologue of the
 RT short PDE4A cAMP-specific phosphodiesterase RD1 (PDE4A1) by analysis
 RT of the human HSPDE4A gene locus located at chromosome 19p13.2.";
 RL Blochem. J. 333:693-703(1998).
 RN [3]
 RP SEQUENCE OF 112-886 FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=90258854; Pubmed=2160582;
 RA Livi G.P., Kmetz P., McHale M.M., Cieslinski L.B., Sathe G.M.,
 RT Taylor D.P., Davis R.L., Torphy T.J., Balcarek J.M.,
 RT "Cloning and expression of cDNA for a human low-km, rolipram-sensitive
 RT cyclic AMP phosphodiesterase.";
 RL Mol. Cell. Biol. 10:2678-2686(1990).
 RN [4]
 RP REVISIONS TO REF.3.
 RA McLaughlin M.M.;
 RL Submitted (JAN-1991) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (PDE4A7/A6 AND PDE4A8/2EL).
 RX MEDLINE=95290008; Pubmed=7772058;
 RA Horton Y.M., Sullivan M., Houslay M.D.;
 RT "Molecular cloning of a novel splice variant of human type IVA
 RT (PDE-IVA) cyclic AMP phosphodiesterase and localization of the gene
 RT to the p13.2-q12 region of human chromosome 19.";
 RL Blochem. J. 308:683-691(1995).
 RN [6]
 RP SEQUENCE FROM N.A. (PDE4A7/A6).
 RX MEDLINE=95194817; Pubmed=7888306;
 RA Sullivan M., Egerton M., Shakur Y., Marguarden A., Houslay M.D.;
 RT "Molecular cloning and expression, in both COS-1 cells and *S.*
 RT cerevisiae, of a human cytosolic type-IVA, cyclic AMP specific
 RT phosphodiesterase (hpde-IVA-h6.1).";
 RL Cell. Signal. 6:793-812(1994).
 CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2O) =
 CC ADENOSINE 5'-PHOSPHATE.
 CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
 CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
 CC -1- SUBCELLULAR LOCATION: THE PDE4A1 RD1 ISOFORM HAS PROPENSITY FOR
 CC ASSOCIATION WITH MEMBRANES.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. PDE46 (SHOWN HERE) REPRESENTS A LONG ISOFORM
 CC AND PDE4A1/RD1 A SHORT ISOFORM. ISOFORM 2EL PROBABLY REPRESENTS A
 CC NON-FUNCTIONAL SPLICE VARIANT. THE PRESENCE OF DIFFERENT N-
 CC TERMINAL REGIONS HAS BEEN LINKED WITH DISTINCT FUNCTIONAL ROLES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L20965; AAA03588.1; -;
 DR EMBL: AF069491; AAC35012.1; JOINED.
 DR EMBL: AF069487; AAC35012.1; JOINED.
 DR EMBL: AF069489; AAC35012.1; JOINED.
 DR EMBL: AF069489; AAC35012.1; JOINED.
 DR EMBL: AF069491; AAC35013.1; JOINED.
 DR EMBL: AF069489; AAC35013.1; JOINED.
 DR EMBL: AF069490; AAC35013.1; JOINED.
 DR EMBL: AF069491; AAC35014.1; JOINED.
 DR EMBL: AF069491; AAC35014.1; JOINED.
 DR EMBL: AF069491; AAC35014.1; JOINED.
 DR EMBL: AF069489; AAC35014.1; JOINED.
 DR EMBL: AF069490; AAC35014.1; JOINED.
 DR EMBL: M37744; AAA69697.1; -;
 DR EMBL: U18087; AAC50458.1; -;
 DR EMBL: U18088; AAA98540.1; -;
 DR EMBL: S75213; AAB33798.1; -;
 DR EMBL: AF069491; AAC35015.1; JOINED.
 DR EMBL: AF069488; AAC35015.1; JOINED.
 DR EMBL: AF069489; AAC35015.1; JOINED.
 DR EMBL: AF069490; AAC35015.1; JOINED.
 DR EMBL: U68532; AAC63832.1; -;
 DR EMBL: U97584; AAC25679.1; -;
 DR PIR: A36317; A36317.
 DR MIM: 600126; -;
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESERASEL.
 DR SMART: SM00471; HDC; 1.
 DR PROSITE: PS00126; PDEASE_1; 1.
 DR HydroLase: CAMP; Alternative
 KW VARSPPLIC 1 107
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRS -> MCFPVTVV (IN ISOFORM PDE4A7/A6).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
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 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
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 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
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 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
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 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
 FT MEPTVSEKSLSLSLPGREGATLKPPQHLMRORPTI
 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
 FT TMOYRSVSEMAHK -> MVLDFECETCSKMLVGMDMO
 FT (IN ISOFORM PDE4A RD1).
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 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
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 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
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 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
 FT SSVTSEAHADLVTPPAQVLASIRVSNFSLITNPVVS
 FT NKRSPLGPPVPCVKAATLSEETCOALAELELDWCLEOLE
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 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
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 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT DSOASPGVLVHAAGATQKRESEFLYRSDSYDMSPKMSN
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 FT RIOGRGSDAEREREROPHRIERADMDTSRPLRT
 FT RMSGPSSFGHTGSGGAGGSSRRFAENGPPSPGRSL
 FT D

Query Match	23.58;	Score 565;	DB 1;	Length 886;
Best Local Similarity	32.18;	Pred. No. 5,5e-38;		
Matches 126;	Conservative 82;	Mismatches 165;	Indels 20;	Gaps
69	VKRLISFGRYEYHNASRLNGILIPQAPRLHLDBEDVYLGQARHMLSKVGMWDEDFLEFRLTNG	128		
Db	332 MSQITGLKMKHMSNSLNNSNIPRGVXTDDELLAELEMLNK--WGLNICVSDYAG	388		
Qy	129 NSLYTLCHLENTFGLIHFKFLDVTYHRLVWVQEDYHSQNYHNAVAADVTQAMHCY	188		
Db	389 RSLTCIMIMIQEEDLLKFKFIPDVTYVWYTLTLEDDHYADVYHNSHAADVLOSTHYL	448		
Qy	189 LKEPLASFLPLDLMIGLLAAAHADVDDHGVQNPFLIKTNHHLADLYOMSVLENHNR	248		
Db	449 LATPLADAVFLDELIALFAAAIHVDVDRHGVSNQFLINTNSLALAMYDESELENHHLA	508		
Qy	249 STIGLRESR--LLAHIPKEMTODIEQGLSLIADINQNFYLTRKALHANO----	302		
Db	509 VGFILQDNDNDIQLNLSKRSQIRKAMVDYAWLADMSKMTLLADLTWTETKRVSS	568		
Qy	303 --LRLEDADRHFMQLAKCADCINPCRIEMSKQSERVCEEPYRGQBLEQKFELETS	360		
Db	569 GVLLDNDSDSDIQLYLRNWHCADISNTKPLEYLRQWTDYIMAEFFQGDREEREMETS	628		
Qy	361 PLCNQOKDSIPISIOIGEMSYIVEPLREFMAHFTGNSTLSENMLGHLAHNKAQMSLL--	417		
Db	629 PMCKRHPTASYKSSQVGFIDYIVHPLMETWMDLVHPD--AOEILDTLEDNRDWYSAIROS	686		
Qy	418 --PROHRSRGSSGSG--PDHHDAGOGGESEEA 446			
Db	687 PSPPEESRSGPHPLPDKFQFELTLEEEEE 719			
RESULT 11				
CN42_RAT	STANDARD;	PRT;	610 AA.	
ID	CN42_RAT			
AC	PI4645;			
DC	01-APR-1990 (Ref. 14, Created)			
DT	01-OCT-1996 (Ref. 34, Last sequence update)			
DEF	15-JUN-1998 (Ref. 36, Last annotation update)			
DE	CAMP-dependent 3',5'-cyclic phosphodiesterase 4A, medium/small			
GN	isoforms (EC 3.1.4.17) (DBPDEZ) (RNPDEFA1).			
OS	PDB4A.			
OC	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NCBI_TaxID	10115;			
RP	SEQUENCE FROM N.A.			
RP	MediLine=95047482; PubMed=7958996;			
RA	Boiger G.B., Rodgers L., Riggs M.;			
RT	"Differential CNS expression of alternative mRNA isoforms of the			
RT	mammalian genes encoding CAMP-specific phosphodiesterases.";			
RL	Gene 149:237-244(1994).			
RP	SEQUENCE FROM N.A.			
RP	MediLine=89264472; PubMed=2542942;			
RA	Davis R.L., Takayasu H., Eberwine M., Myers J.;			
RT	"Cloning and characterization of mammalian homologs of the Drosophila			
RT	Proc. Natl. Acad. Sci. U.S.A. 86:3604-3608(1989).			
RP	SEQUENCE OF 84-442 FROM N.A.			
RP	TISSUE-Testis;			
RA	MediLine=89315790; PubMed=2546153;			
RA	Swinnen J.V., Joseph D.R., Conti M.;			
RT	"Molecular cloning of rat homologues of the Drosophila melanogaster			
RT	dunce CAMP phosphodiesterase: evidence for a family of genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).			
RP	STRUCTURE BY NMR OF 1-26.			
RP	MediLine=96279244; PubMed=8663181;			

RA Smith K.: Scotland G. Beattie., Tryer I.P. Houslay M.D.;
RT "Determination of the structure of the N-terminal splice region of
RT the cyclic AMP-specific phosphodiesterase RDL (RNPd441) by 1H NMR
RT and identification of the membrane association domain using chimeric
RT constructs";
RL J. Biol. Chem. 271:16703-16711(1996);
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED
CC BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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DR EMBL: L27062; AAA56859.1; -
DR EMBL: M25348; AAA1848.1; -
DR EMBL: M28411; AAA1823.1; -
DR EMBL: M28715; AAC37689.1; -
DR EMBL: M28715; AAA41101.1; -
DR EMBL: M28717; AAA41102.1; -
DR PIR: B33904; B33904.
DR PIR: A32558; A32558.
DR PIR: ILOI; I5-MAY-97.
DR Interpro: IPR003607; HDC.
DR Interpro: IPR002073; PDase.
DR Pfam: PF00233; PDase.1
DR PRINTS: PR00387; PD1ESTERASE1.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDASE-1; 1.
DR Hydroxylase: CAMP; Alternative splicing; Multigene family; 3D-structure.
FW DOMAIN 466 471 POLY-GLU.
FT VAAPSLIC 1 25 MISSING (IN MEDIUM ISOFORM).
FT VAAPSLIC 1 84 MISSING (IN SMALL ISOFORM).
FT VAAPSLIC 120 152 MISSING (IN SMALL ISOFORM).
FT CONFLICT 231 232 MISSING (IN SMALL ISOFORM).
FT CONFLICT 369 370 GV -> AL (IN REF. 3).
FT CONFLICT 599 599 GD -> AH (IN REF. 3).
FT CONFLICT 599 599 A -> T (IN REF. 2).
SQ SEQUENCE 610 AA; FE439ACE95E1DIAC CRC64;
Query Match 23.2%; Score 559.5; DB 1; Length 610;
Best Local Similarity 31.1%; Pred. No. 9.2e-38;
Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;
OY 43 RGSVPFIDFLPLNSTYSGEIGTKKKVVRLLSFQYFPAFLSLGIIIPQARLLDDEVL 102
DB 80 RQSPSPQIIGLKKLVITGSLNTN-----VPRGVTQDEDL 117
OY 103 GQAHMISKSGMDDPFLFEDRLITGNSLITLLCHLEFTHGILNHFKLDVTLRFLVAV 162
DB 118 AQELENLSK---WGLNIFCVSEYAGRSLSCTIMTITFERDLKKFHFIVDTMMITML 174
OY 163 QEDYHSNPYHNAVHADYQAMHCCYKPKLASFLRPLDTMLGLLAAAHADVDRPGVNO 222
DB 175 EDHHAHVAUHNLSHADYLOSTHYLLATPALDAVFTDLETLAALFAAAIHVDVDRGVSN 234
OY 223 PELIKTNHILANLYQMSVLENNHNRSTIGMLRESR--LAAHFKREMTODIEOGLSL 280
DB 235 QELINTNSELALYNDSEVLENHNLAVGFKLLDQENCDFIQNSKROROSTLRKIVDYL 294
OY 281 ATDINRNEFLTYLKAHLHNKD-----LRLEDADDRHFMIQALKAADICNCRITWES 334
DB 295 ATDMSKIMTLADLKTMYETKRVTSQVLLLDNTNSDRIOYLRNNWBCADLSNPTKPLELY 354

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QY 335 KQMSRVCVEEZYRQGELEQKTELEISPLCNOQKSIPTSIQIGFMSYIVERPLFRWMAHFTG 394
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 355 RQMTDRIAEFFQOQDGRERERGERMEISPMCKHTFASVSKSGVGFIDYIVHPLMETWADLVH 444
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
QY 395 NSTLSENNLGLHLANKQWKSLPLRQHRKRSSSGF-DHIDHAGQ-----TE 441
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 415 PD-AODLIDTLEDDR-DW-----YHSALRQSPSPLEERPGGIGHPSLPDKQFELTL 465
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
QY 442 SEQEGDS 449
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 466 EEEEEEDS 473
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

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RESULT 12
ID      CN4A_RAT          STANDARD:          PRT;      844 AA.
AC      P54748;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      cAMP-dependent 3',5'-cyclic phosphodiesterase 4A, large isoforms
DE      (EC 3.1.4.17) (PDBEZ).
GN      PDE4A.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=95047482; PubMed=7958996;
RA      Bolger G.B., Rodgers L., Riggs M.;
RT      "Differential CNS expression of alternative mRNA isoforms of the
RL      mammalian genes encoding cAMP-specific phosphodiesterases.";
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 8).
RC      STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX      MEDLINE=96132847; PubMed=8557632;
RA      Bolger G.B., McPhée I., Houslay M.D.;
RT      "Alternative splicing of cAMP-specific phosphodiesterase mRNA
RT      transcripts. Characterization of a novel tissue-specific isoform,
RL      RNDE4A8.";
RN      J. Biol. Chem. 271:1065-1071(1996).
CC      -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC      ADENOSINE 5'-PHOSPHATE.
CC      -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC      -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC      -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED
CC      BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: ISOFORM 8 IS PRESENT ONLY IN TESTIS.
CC      -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC      FAMILY.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR      EMBL; L27057; AAC27098.1; -.
DR      EMBL; L36467; AAB00357.1; -.
DR      InterPro; IPR003607; HDC.
DR      InterPro; IPR002073; PDase.
DR      Pfam; PF00233; PDase.1.
DR      PRINTS; PRO0387; PDSESTERASE1.
DR      SMART; SMO0471; HDC.1.
DR      PROSITE; PS00126; PDASE_1; 1.
KW      Hydrolase; cAMP; Alternative splicing; Multigene family.
FT      VARSPIC 1 102

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FT	FT	SO	SEQUENCE	844 AA;	93438 MW;	1A5F5101EADBFB1B6 CRC64;	RMSWPSSFHGTGGSSRR -> MPRKRLTLPRFIYRKK NGNS (IN ISOFORM 8).

Query Match	23.28;	Score 559.5;	DB 1;	Length 844;
Best Local Similarity	31.18;	Pred. No. 1.4e-37;		
Matches 133;	Conservative 77;	Mismatches 163;	Indels 55;	Gaps 9;

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OY 43 RGSVFEIDFRLNSTRVTSSELGKTKKYYKRLSPORFYHNSALRGIIIPQARPHILNDEYU 102
Db 314 ROSQMSOITGKLKLVHTGSLNT-----VPRRGVKTDOEDL 351
OY 103 GOARHLSTKVQMWDFLEFEDRLTNGNSLYLTLCHEPNTGLIHNFELKIDVTLRELVUV 162
Db 352 AQELENLSK----WGILNIPCVSEYAGNRSLSOIMTIIOERDLKLFHIIIPVTMMYMLT 408
OY 163 QEDHNSQNPYNAAVADYTOAMHCYKKEPKLASFTLRPLDMLGLAAAHDVDHPVNO 222
Db 409 EDHYIADVAHYNSHSLAADVLOSTHYLLATPRLADVNFUDELIALFMAAIIHDYDHPVSN 468
OY 223 PELIKTNNHLNVLQNSVSLNHNHMRSTIGMLRESR--LIANHPKEMTODIEOGLSTL 280
Db 469 OFLITNTSELMLMNDSEVLNHNHLANGFKLLDQENCDIFONLSKROQSLRKVYIDMYL 528
OY 281 ATDINRONEFLTRKAILHNKD-----LRLEDAQDRHFMLOIALKCADICNPCRITWMS 334
Db 529 ATDMSKHNHTLADLKTWETKKYTSGLVLLDNDSDRIQVLRNNVHCADLSNPTKPELY 588
OY 335 KQMSRVCEERYRQGELOKFELEISPLCNQOKSISISIQGMSYIYERFLRMAFTG 394
Db 589 KQMDIRIAEEFQOQDREREGEMETSPKCDNHTSVESQUGFIDUYIVNPLMETMADLVH 648
OY 395 NSTSENNMLGHLHNKAKQMSLLPRONHSGSSGGR-DHDAQOG-----TE 441
Db 649 PD-AQDLIDLTLLENR-DW-----YHAIQNSPRLPEERPGGLGHSRLPDKQFELTL 699
OY 442 SEEDGDS 449
Db 700 EEEEDDS 707

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RESULT	13
CN4C_HUMAN	
ID	CN4C_HUMAN
AC	Q08493;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, last sequence update)
DT	30-MAY-2000 (Rel. 39, last annotation update)
DE	CAMP-dependent 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE	(PDE4).
GN	PDE4C.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (PDE4C1).
RC	TISSUE=Substantia nigra;
RX	MEDLINE=95145731; PubMed=7843419;
RA	Engels P., Sullivan M., Mueller T., Luebbert H.;
RT	"Molecular cloning and functional expression in yeast of a human
RT	CAMP-specific phosphodiesterase subtype (PDE IV-C).";
RL	FEBS Lett. 358:305-310(1995).
RN	[2]
RP	SEQUENCE OF 462-712 FROM N.A.
RX	MEDLINE=94019330; PubMed=8413254;
RA	Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
RA	Rodgers L., Riggs M., Wiegler M., Ferguson K.;
RT	"A family of human phosphodiesterases homologous to the duncer
RT	learning and memory gene product of <i>Drosophila</i> melanogaster are
RT	potential targets for antidepressant drugs.";
RL	Mol. Cell. Biol. 13:6558-6571(1993).

CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF THE PROTEIN (PDE4C1 TO
CC PDE4C7) ARE PRODUCED BY ALTERNATIVE SPLICING. THE ISOFORM SHOWN
CC HERE IS PDE4C1.
CC TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES BUT NOT IN CELLS
CC OF THE IMMUNE SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC -----
DR EMBL: 246632; CAA86601.1; -
DR EMBL: L20968; AAA03591.1; -
DR MIM: 600128; -
DR InterPro: IPR003607; PDC.
DR InterPro: IPR002073; PDCase.
DR Pfam: PF00233; PDCase; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDCASE; 1.
KW Hydrolyase; CAMP, Multigene family; Alternative splicing.
SQ SEQUENCE 712 AA; 79845 MW; 0EC70E917A393F78 CRC64;

Query Match 23.0%; Score 553; DB 1; Length 712;
Best Local Similarity 27.8%; Pred. No. 3.8e-37;
Matches 135; Conservative 94; Mismatches 198; Indels 58; Gaps 10;

QY 11 ELLEPNDONAKCVMGDIRLGOTGYAERGSYPFIDRLIN-----STTYSG- 61
DB 204 KLALETLDLWCLDLETLQTRHSVGEASNFK-----RIINRELTHLSETRSGNQ 257
QY 62 -----EIGTKK-----KVKRLSFQRYFASRLNGIIPQAPLHIDE 99
DB 258 VSEYISRTFLDQOTEVELPKYAEBAPOMSRISGHLGHSASLSATVPREFGVTDQE 317
QY 100 DYLGQARHMLSKVGMDFPIFLFDRLTNGNSLVTLCLHFTNHLGHHFKIDVTLHRL 159
DB 318 EQLAKE--LEDTNKMGDLVFKVADVSGNRPFLTAIFISFQERDLTKTFQIPADTLATYL 374
QY 160 VMVOEDYHSQNPYHNNAVHADYTOAMHCYLKEPKLASFLPRLDIMGILAAAHVDVHPG 219
DB 375 LMEGHYHANVAVYHNSIHADYVOSTHYVLATPRALEAVFTDLELALFSAIHVDVHPG 434
QY 220 VNPELLIKNNHNLAYOMSYLENHMKRSTIGMRER--LNAHLKREMTQDIEOOLGS 277
DB 435 VSNQFLITNSDVALMTNDASVLENHNLAVGFKLDAENCDFONLSAKORLSRRWVD 494
QY 278 LLIATDINQNEFLRLKAHLHMKD-----LRLEDAQDRHFMQLAKACADICNCRW 331
DB 495 MVTATMSKHMNLADLKLMTVEFKVTSIGVLLDNDYSDRLOVQNLNVHCAADLSNPKPL 554
QY 332 ENKMSQSERVCEEFYRQGLERKFLPETSPLCNOOKDISPISQIFGMSYVEPLFRMAH 391
DB 555 PLRWMTDRIMAEFFQOGRERESGLDISPMCDKHTASVEKSGYGFIDYIAHPLMETWAD 614
QY 392 FTGNSLSTENMLGHLAHNAOKWSLIPROHRS-RGSSGSGGDH-----DHAGQGESE 443
DB 615 LVHPD--AODLDTLEDNRNEMVQSKIPRSPDLTPNRPDGRDROFETLLEAEEDDEE 672
QY 444 EOEKG 448
DB 673 EEEGE 677

RESULT 14
CNC_C_RAT STANDARD; PRT; 536 AA.
ID CNC_C_RAT
AC P1644;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-dependent 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE (PDE4C) (Fragment).
GN PDE4C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95047482; Pubmed-7958996;
RA Bolger G.B., Rodgers L., Riggs M.;
RT "Differential CNS expression of alternative mRNA isoforms of the
RT mammalian genes encoding CAMP-specific phosphodiesterases.";
RL Gene 149:237-244 (1994).
NR [2]
RP SEQUENCE OF 153-511 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-89315790; Pubmed-2546153;
RA Swinnen J.V., Joseph D.R., Conl M.;
RT Molecular cloning of rat homologues of the Drosophila melanogaster
RT dunce CAMP phosphodiesterase: evidence for a family of genes.;
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329 (1989).
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC -----
DR EMBL: L27061; AAA56858.1; -
DR EMBL: M25347; AAA1847.1; -
DR PIR: A33904; A33904.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002073; PDCase.
DR Pfam: PF00233; PDCase; 1.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDCASE; 1.
KW Hydrolyase; CAMP, Multigene family.
FT DOMAIN 1
FT DON_TER 1
FT FT 524 534 POLY-GLU.
FT CONFLICT 218 218 R -> S (IN REF. 2).
FT CONFLICT 507 507 S -> N (IN REF. 2).
SQ SEQUENCE 536 AA; 60063 MW; 87D12BE2C46642F3 CRC64;

Query Match 22.0%; Score 529.5; DB 1; Length 536;
Best Local Similarity 30.8%; Pred. No. 2.1e-35;
Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;

QY 71 RLSEFYFASRLRRIIPQAPLHLDYDYGQARHMLSKVGMDFPIFLFDRLTNGNS 130
DB 156 QITGLRKSCHTS-LPRAIDPRFGVGTDEQELAKE--LEDTNKMGDLVFKVAVELSGRRP 211
QY 131 LVTLCLHFLNTHGILNHFKIDVTLHRLVMVOEDYHSQNPYHNNAVHADYTOAMHCYLK 190
DB 212 LTAIVIFRVLQERDLTKTFQIPADTLRLRYLTLEGHTHNSVAVYHNSIHADYVQSAHYLLG 271

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:01:39 : Search time 16.3 Seconds
(without alignments)
674.326 Million cell updates/sec

Title: US-09-471-459A-5
Perfect score: 2408
Sequence: 1 MSCLMVCKRCGEILFENPDON.....PDHHDAGCGTESEEGEDSP 450

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2258	93.8%	502	US-09-330-970-1	Sequence 1, App11
2	1419.5	58.9	498	US-07-688-352C-20	Sequence 20, App1
3	1419.5	58.9	498	US-08-474-379C-20	Sequence 20, App1
4	1419.5	58.9	498	US-09-146-249A-20	Sequence 20, App1
5	1419.5	58.9	498	US-08-206-188B-20	Sequence 20, App1
6	1280	53.2	320	US-09-330-970-3	Sequence 3, App11
7	604.5	25.1	673	US-08-474-379C-63	Sequence 63, App1
8	604.5	25.1	673	US-09-146-249A-63	Sequence 63, App1
9	599.5	24.9	673	US-08-206-188B-63	Sequence 63, App1
10	599.5	24.9	673	US-08-577-492-35	Sequence 35, App1
11	599.5	24.9	673	US-09-079-630-35	Sequence 35, App1
12	580.5	24.1	562	US-07-688-352C-4	Sequence 4, App11
13	580.5	24.1	562	US-08-942-521B-8	Sequence 8, App11
14	580.5	24.1	562	US-08-474-379C-4	Sequence 4, App11
15	580.5	24.1	562	US-09-146-249A-4	Sequence 4, App11
16	580.5	24.1	562	US-08-206-188B-4	Sequence 4, App11
17	580.5	24.1	562	PCT-US91-02714-4	Sequence 4, App11
18	567.5	23.6	564	US-08-577-492-34	Sequence 34, App1
19	567.5	23.6	564	US-08-942-521B-2	Sequence 2, App11
20	567.5	23.6	564	US-08-474-379C-59	Sequence 59, App1
21	567.5	23.6	564	US-09-146-249A-59	Sequence 59, App1
22	567.5	23.6	564	US-08-206-188B-59	Sequence 59, App1
23	567.5	23.6	564	US-09-192-702-2	Sequence 2, App11
24	567.5	23.6	564	US-09-079-630-34	Sequence 34, App1
25	567.5	23.6	564	US-08-445-474-2	Sequence 2, App11
26	567.5	23.6	564	PCT-US94-02612-2	Sequence 2, App11
27	567.5	23.6	736	US-07-688-352C-24	Sequence 24, App1

28	567.5	23.6	736	US-08-474-379C-24	Sequence 24, App1
29	567.5	23.6	736	US-09-146-249A-24	Sequence 24, App1
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31	567.5	23.6	736	PCT-US91-02714-23	Sequence 23, App1
32	565	23.5	885	US-08-577-492-33	Sequence 33, App1
33	565	23.5	885	US-09-079-630-33	Sequence 33, App1
34	565	23.5	886	US-08-474-379C-65	Sequence 65, App1
35	565	23.5	886	US-09-146-249A-65	Sequence 65, App1
36	565	23.5	886	US-08-206-188B-65	Sequence 65, App1
37	563	23.4	666	US-08-942-521B-9	Sequence 9, App11
38	562	23.3	606	US-08-577-492-32	Sequence 32, App1
39	562	23.3	606	US-09-079-630-32	Sequence 32, App1
40	560.5	23.3	404	US-08-474-379C-44	Sequence 44, App1
41	560.5	23.3	404	US-09-146-249A-44	Sequence 44, App1
42	560.5	23.3	404	US-08-206-188B-44	Sequence 44, App1
43	559.5	23.2	610	US-08-974-565C-9	Sequence 9, App11
44	559.5	23.2	610	US-09-255-748-9	Sequence 9, App11
45	558.5	23.2	481	US-08-286-856C-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-09-330-970-1
; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ. ID NOS.: 40
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-1

Query Match 93.8%; Score 2258; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.8e-229;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	28	GDRLRGQTVRAERKSGYFIDRLINSTTYSGETGKTKKVKRLSFQRYFNASRLRG	87
DB	80	GDRLRGQTVRAERKSGYFIDRLINSTTYSGETGKTKKVKRLSFQRYFNASRLRG	139
QY	88	IIPQAPRLHLDDEYLGARHMLSVGMWDFDLEFDRLTGNSLVTLCHLFNTHGIIH	147
DB	140	IIPQAPRLHLDDEYLGARHMLSVGMWDFDLEFDRLTGNSLVTLCHLFNTHGIIH	199
QY	148	FKIDMTVLRFLVWQEDYSQNPYHNAVADVTQAMHCYLEKPKLASFTPLDITMGL	207
DB	200	FKIDMTVLRFLVWQEDYSQNPYHNAVADVTQAMHCYLEKPKLASFTPLDITMGL	259
QY	208	LAADHDVDPGVNOPELITNNHNLAYONMSVLENHNRSTIGMLRESRLAHLPEKEM	267
DB	260	LAADHDVDPGVNOPELITNNHNLAYONMSVLENHNRSTIGMLRESRLAHLPEKEM	319
QY	268	TDIDEOGLSLIATDINRQNEFLTRKALHKKDLRLDQADRHFMLOTATACADICNP	327
DB	320	TDIDEOGLSLIATDINRQNEFLTRKALHKKDLRLDQADRHFMLOTATACADICNP	379
QY	328	CRIMWKSQSEVCEEFYRQGELEOFLEISPLCNOQKDSIPSIOIGFMSYIVPELFR	387

Db 380 CWMGSKWSEVCEEFYRGGELEFQFELEISPLCNOOKDIPSQIGEMSYVEPLR 439
QY 388 EAAHTGNSSTLSENNLGHLANHKAQWKSLLPROHRSKSSGSGPDHDHAGQTESEORC 447
Db 440 EAAHTGNSSTLSENNLGHLANHKAQWKSLLPROHRSKSSGSGPDHDHAGQTESEORC 499
QY 448 DSP 450
Db 500 DSP 502

RESULT 2
US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 964-5740
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-688-352C-20

Query Match 58.9%; Score 1419.5; DB 1; Length 498;
Best Local Similarity 61.7%; Pred. No. 1,3e-140;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

Db 7 ERGCGILEFNDQNAKCMGIDRLRGQGVRAERKSGPFDIFLNLSTYSGEIGTK 66
QY 62 ORRGAISTDSSDQALYRLMGIDVRVRSGFESERKSHPIYDFRIFHSQSEIEVSVA 121
Db 67 KKKVRLSFGYRFHASRLRGIIIPQAPLHLDEDIYLGQARHMLSKVGMDEDFLEDRLT 126
QY 122 NRIKRLSFGYRLSRRFRTAVSNLNLIDDDYNGQAKMDEKVGNNPFIPLFDRLT 181
Db 127 NNSLVTLCHLFTNGLIHFKLDMVTLHFLVWQEDVHSONPYHNAVHADVYQAAH 186
QY 127 NNSLVTLCHLFTNGLIHFKLDMVTLHFLVWQEDVHSONPYHNAVHADVYQAAH 186

Db 182 NNSLVSLTFHFLSLHGLIEYHLDMLKRLRPELVYIOEDYHSONPYHNAVHADVYQAAH 241
QY 187 CYLKEPKLASFLTPDLIDMIGLLAAAHVDHPGVNOPELITKTNHNLNLYONNSVLENH 246
Db 242 CYLKEPKLANSVYVPDWILSLIAAATHDLDHGVNOPELITNTNLYLTLYLNKNSVLENH 301
QY 247 WRSTIGMLRESRLLAHLPEKEMTODIEQOLGSLIATDINRONEFLTRKAHLNKLRL 306
Db 302 WRSVGLRESGLFSLHPLPESRQOMETOIGALIIATDISRONEFLSFRSLRDICLE 361
QY 307 DAODRHFMLQIALKADICNPICRIMESKOWSERVCEEFYRGGELEFQFELEISPLCNOQ 366
Db 362 DTRHRLHYLQMALKCADICNPCTRWELEKOWSEKVTLEEFHQDIEKKYHGVSLCDRH 421
QY 367 KDSIPSTOIGFMSYIYEPLEFREMHTGNSSTLSENNLGHLANHKAQWKSLLPROHRSRG 426
Db 422 TESTANIQGFMYLVEPFTEMARFS-NTRLSTGMCHGVNLNASKGGLQROSSSEDT 480
QY 427 SGS 429
Db 481 DAA 483

RESULT 3
US-08-474-379C-20
; Sequence 20, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-474-379C-20

Query Match	58.9%;	Score 1419.5;	DB 2;	Length 498;
Best Local Similarity	61.7%;	Pred. No. 1.3e-140;		
Matches 261;	Conservative 70;	Mismatches 91;	Indels 1;	Gaps 1

QY	7	ERCEIIEFNEDONAKCYCMJGDI:RLRGQTVRAERNGSYFIDFRLN:STTYSGEIGTK	66
Db	62	ORRGAI:YDSSDQYALYIRMLGDYRVRSRAQFESRRSGSHYIDPRIFHSO:SEIEVSVA	12
QY	67	KKVRLLSFOYRPHASRLRGITPOAP:HLHLDDEDYLGARHMLSKVGMDFIDLEDRLT	12
Db	122	RNIRLLSFORYLKRSSRFRCTAVSNS:LNIIIDDDYNGCAKMLKEVGMWNEPDI:FEFRLT	18
QY	127	NGNSJVTLLCHLFPHNGIHHFKIDMYL:HLHFELWQVDYSONPYHNAVAADYQAMH	18
Db	182	NGNSJVSJLTFHFLES:HGILLEYFILDMMKLRFFLVMIQEDYSONPYHNAVAADYQAMH	24
QY	187	CYLKEPKLASRLT:PLDILMGLAAAHHDVDPGVQNPFLITNHHLANIYOMNSYLENNH	24
Db	242	CYLKEPKLASVNT:PMWIDILSLAAATHDLDH:PGVQNPFLITNHYLATLYKNTSVLENHH	30
QY	247	WRSTIYGMRESRL:LANHPKEMTQDIEOQSLIATIDINRONNEFLTRKALH:HNKDLRLE	30
Db	302	WRSVAGLL:REGSLFHSHPLESROOMETOIGALLIATDISRONEYLS:FRSHLDRODLCLE	36
QY	307	DAORHFMILAT:ALCADI:CNPCRIEMKSKOMSERVCEEFYQSGE:LEOKFELIEISPLCNOQ	36
Db	362	DTNRHHVLQWAL:KACADICNPCRIMWELSKOMSEKTEFEFFHQGDLEKTYHILGVSPLCRH	42
QY	367	KDSIPS:IDIGMASYI:VEPDLFREMNAHFTGNSITLSENMLGHLA:HNKAMKSLRPHORHSRG	42
Db	422	TESIANIQIGEMTYL:VEPDLFTEMARFS-NTRLSQMGILGHVGNKASMGKLG:ROESSSEDT	48
QY	427	SGS 429	
Db	481	DAA 483	

RESULT 4
US-09-146-249A-20
Sequence 20, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448

```

:          TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 20::
:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 498 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:
: US-09-146-249A-20

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Query Match	58.9%;	Score 1419.5;	DB 3;	Length 498;
Best Local Similarity	61.7%;	Pred. No. 1.3e-140;		
Matches 261;	Conservative 70;	Mismatches 91;	Indels 1;	Gaps 1;

QY	7	ERCEIILEFNDPONAKVCMIJGDIRRGOTGVAAERRSYSPFIDRLLNSTYSGEIGTK	66
Db	62	ORRGAISYSSDDOTALYIRMLGDVVRVSRAGFESEKRSHPYIDFRIPHSOSELIVSVA	121
QY	67	KKVKRLLSFORYFNHASNLLNGITTPQAPRHLHDEDDYIGCARHMLSKVGMDFDIFDRLT	126
Db	122	RNIRRLLSFORYLRSSFFRFGTAVSNSLTLDDDDYNGQAKCMLEKGMNPFIDFLDRLT	181
QY	127	NGNSLVTLTLOHLPNTGHLHFKLDWVTLHRFLVWVOEYHSONPRYHNAVHAADYTOAMH	186
Db	182	NGNSLVSLTHTLHSLHGLIYFHLIDMKLRLRLVLMIOEDYHSONPRYHNAVHAADYTOAMH	241
QY	187	CYLKEPKLASFLTRPLDMLTGLAAAAADVDHPGVNOPLFKITNHLIANLYOMSVLENHH	246
Db	242	CYLKEPKLASVYRPWDLTSLIAAATCHDDHDHPGVNOPLFKITNHYLATLTKNTSVLENHH	301
QY	247	WRSTIGMLRSLRLAHNPKEMTODIEQOGLSLIADDIRKOWNEFLTRKANHANNDDYLE	306
Db	302	WRSAVGLRRESGSHLPSLPSRROOMETOGALLIADIRONEVYSLERSHDDRODLCLE	361
QY	307	DAODRHMILIAKCADICNPRCIWEMSKOWSERVCEEFYRGGELQEFKELEISPLCNOQ	366
Db	362	DTIRRHLYLQALMKCADICNPRCTWELSMOWMSKYVEEFPFHOGDIEKKYHILGVSPDCORH	421
QY	367	KDSLPISQICPMSTIYEPFLREKANAHTGNSSTSENMLGHLAHNKAOWMSLDRQHRSGS	426
Db	422	TESIANIQIOMFYLEPFLTEWARFS-NTRLSOTMIGHYGNKASWKLOAREOSSSEDT	480
QY	427	SGS	429
Db	481	DAA	483

RESULT 5
US-08-206-188B-20
Sequence 20, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994

Mon Sep 16 16:41:06 2002

us-09-471-459a-5.rai

Page 4

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? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/511,715
? FILING DATE: 20-APR-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: CLOUGH, David W.
? REGISTRATION NUMBER: 36107
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6300
? TELEFAX: 312/474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ. ID NO.: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 498 amino acids
? type: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-206-188B-20

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-63

Query Match 25.1%; Score 604.5; DB 2; Length 673;
Best Local Similarity 33.3%; Pred. No. 9.9e-55;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPLHLDEDEYLGQARHMLSKVGMDFDIFL 121
DB 218 KKKKKRPMQISGVKKLMHSSSLTNSIPFGVKTQEDVLAKE--LEDVNMKGLHVR 274
QY 122 FDRLTNGSLVTLTLC-LFNTHGLIHFKLDVTLHRLVMOVQEDYHSQNPYNAVAHAD 180
DB 275 IAEI-SGNRPVLYIMHTIFQERDLTFKIPVDTLITYLTLEDYHADVAHNNIHAAD 333
QY 181 VTQAMCYLKEPKLASFLPLDMLGLAAAHADVDPGVNOPLFKITNHLNLYQNM 240
DB 334 VQSTHVLSTPALAEVFDLELAIFASAIHDVDPGVSNQFLINTSELAAMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LLAHLPEMTQDIEQGLSLATDINRONEFLTRKALH 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKORSLRKWVIDIVLATDMSKHNMLADLKTWV 453
QY 299 HNND-----LRLEDAODRHFMLOIALKCADICNPCRIMESKOWSERVCEERYGGELE 352
DB 454 ETKKVTSSGVLLDNTSDRIQVLYQNNVHCADLSNPKPLQVLRQMDRIEMEEFRGQDRE 513
QY 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIPELRFREMAHFTGNSLSENNLGHANAKQ 412
DB 514 RERGMEISPMCKHNASVEKSGVFIDYIVHPLMETWADLVHPD--AQDILDTLEDNRBW 571
QY 413 WKSLPRQHRSRGSSGCPDHAGGCTESE-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEEGROGOTEKQFELTLEEDGS 610

RESULT 8
US-09-146-249A-63
Sequence 63, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715

FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-146-249A-63

Query Match 25.1%; Score 604.5; DB 3; Length 673;
Best Local Similarity 33.3%; Pred. No. 9.9e-55;
Matches 135; Conservative 86; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPLHLDEDEYLGQARHMLSKVGMDFDIFL 121
DB 218 KKKKKRPMQISGVKKLMHSSSLTNSIPFGVKTQEDVLAKE--LEDVNMKGLHVR 274
QY 122 FDRLTNGSLVTLTLC-LFNTHGLIHFKLDVTLHRLVMOVQEDYHSQNPYNAVAHAD 180
DB 275 IAEI-SGNRPVLYIMHTIFQERDLTFKIPVDTLITYLTLEDYHADVAHNNIHAAD 333
QY 181 VTQAMCYLKEPKLASFLPLDMLGLAAAHADVDPGVNOPLFKITNHLNLYQNM 240
DB 334 VQSTHVLSTPALAEVFDLELAIFASAIHDVDPGVSNQFLINTSELAAMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LLAHLPEMTQDIEQGLSLATDINRONEFLTRKALH 298
DB 394 VLENHNLAVGFKLQENCDIFQNLTKKORSLRKWVIDIVLATDMSKHNMLADLKTWV 453
QY 299 HNND-----LRLEDAODRHFMLOIALKCADICNPCRIMESKOWSERVCEERYGGELE 352
DB 454 ETKKVTSSGVLLDNTSDRIQVLYQNNVHCADLSNPKPLQVLRQMDRIEMEEFRGQDRE 513
QY 353 QKFELEISPLCNOQKDSIPSIQIGFMSYIPELRFREMAHFTGNSLSENNLGHANAKQ 412
DB 514 RERGMEISPMCKHNASVEKSGVFIDYIVHPLMETWADLVHPD--AQDILDTLEDNRBW 571
QY 413 WKSLPRQHRSRGSSGCPDHAGGCTESE-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEEGROGOTEKQFELTLEEDGS 610

RESULT 9
US-08-206-188B-63
Sequence 63, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-188B-63

Query Match 25.1%; Score 604.5; DB 3; Length 673;
Best Local Similarity 33.3%; Pred. No. 9,9e-55;
Matches 135; Conservative 66; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKVKRLS----FQRYFHASRLRLGIIIPQAPRLHLLDEYLGQARHMLSKVGMDFDIFL 121
DB 218 KKKRRPMSQISGVKLMHSSSLNSSIPRGVKTQEDVLAKE--LEDVKNMGILHVR 274
QY 122 FDRLTNGNSLVTLCH-LFNTNGLIHFKLDVTLHREFLVMVOEDYHSQNPYHNAVHAAD 180
DB 275 IAEI-SGNRPULTVIMHTIFQERDLTKFKIPVDTLTLYMTLEDHNAVAHANNHINHAAD 333
QY 181 VTQAHCYLKEPKIASFLTPDLMGLAAADVDHPGVNOFPLIKTNHNLANLYONNS 240
DB 334 VVOSTHVLSTPALEAVFTDLEILAAIFASAIHDVHPGVSNOLFINTSELAIMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LNAHLPKEMTODIEOGLSLIATDINRONEFLTRLKAHL 298
DB 394 VLENHNLAVGFKLLQENCDIFQNLTKKQKQSLRKMYIDIVLATDMSKHMNLADLKTMY 453
QY 299 HNKD-----LRLEDAODRHFMQLALCKADICNPCRIMESKOMSERVCEFFYRQGELE 352
DB 454 ETKKVTSSGYLLDNYSDRIQVLYNNVHCADLSNPTKPIQLYRQMTDRIMEEFFRQGRE 513
QY 353 OKFLEISPLCNOKDSIPSIQIGFMSYIYEPFLREMAHFTGNSLSENNGLAHNKAQ 412
DB 514 RERGMEISPMQDKHNAVEKSYGVGFDIYVHPLMETWADLVHPD--AQDILDTLEDNRNW 571
QY 413 WKSLPRQHRSGSSGSGPDHNAOGTSESE-----EQEGDS 449
DB 572 YQSTIRPQ-----SPSPAPDDPEGRGQGTGRKQFELTLEEDGES 610

RESULT 10
US-08-577-492-35
Sequence 35; Application US/08577492
Patent No. 5851784
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784aris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/577,492
FILING DATE: 22-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-577-492-35

Query Match 24.9%; Score 599.5; DB 2; Length 673;
Best Local Similarity 33.6%; Pred. No. 3,3e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;

QY 66 KKKVKRLS----FQRYFHASRLRLGIIIPQAPRLHLLDEYLGQARHMLSKVGMDFDIFL 121
DB 218 KKKRRPMSQISGVKLMHSSSLNSSIPRGVKTQEDVLAKE--LEDVKNMGILHVR 274
QY 122 FDRLTNGNSLVTLCH-LFNTNGLIHFKLDVTLHREFLVMVOEDYHSQNPYHNAVHAAD 180
DB 275 IAEI-SGNRPULTVIMHTIFQERDLTKFKIPVDTLTLYMTLEDHNAVAHANNHINHAAD 333
QY 181 VTQAHCYLKEPKIASFLTPDLMGLAAADVDHPGVNOFPLIKTNHNLANLYONNS 240
DB 334 VVOSTHVLSTPALEAVFTDLEILAAIFASAIHDVHPGVSNOLFINTSELAIMYNDSS 393
QY 241 VLENHNRSTIGMLRESR--LNAHLPKEMTODIEOGLSLIATDINRONEFLTRLKAHL 298
DB 394 VLENHNLAVGFKLLQENCDIFQNLTKKQKQSLRKMYIDIVLATDMSKHMNLADLKTMY 453
QY 299 HNKD-----LRLEDAODRHFMQLALCKADICNPCRIMESKOMSERVCEFFYRQGELE 352
DB 454 ETKKVTSSGYLLDNYSDRIQVLYNNVHCADLSNPTKPIQLYRQMTDRIMEEFFRQGRE 513
QY 353 OKFLEISPLCNOKDSIPSIQIGFMSYIYEPFLREMAHFTGNSLSENNGLAHNKAQ 412
DB 514 RERGMEISPMQDKHNAVEKSYGVGFDIYVHPLMETWADLVHPD--AQDILDTLEDNRNW 571
QY 413 WKSLPRQHRSGSSGSGPDHNAQ-OGTSESE-----EQEGDS 449
DB 572 YQSTIRPQ-----SPSPAPDDPEGRGQGTGRKQFELTLEEDGES 610

RESULT 11
US-09-079-630-35
Sequence 35; Application US/09079630
Patent No. 6291199
GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Perry, Martin John
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
NUMBER OF SEQUENCES: 40

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
;; STREET: One Liberty Place, 46th floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/079,630
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/577,492
;; FILING DATE: 22-DEC-1995
;; APPLICATION NUMBER: GB 9426227.6
;; FILING DATE: 23-DEC-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9512996.1
;; FILING DATE: 26-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cherry, David A.
;; REGISTRATION NUMBER: 35,099
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 673 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;;
US-09-079-630-35

Query Match 24.9%; Score 599.5; DB 4; Length 673;
Best Local Similarity 33.6%; Pred. No. 3.3e-54;
Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;
QY 66 KKKVKRLS---FQRYFNASRLRLGIIIPQAPRLHLLDEVDYLGQARHMLSKVGMWDDIFL 121
DB 218 KKKKKRPMQISGVKKLMHSSSLNNSIPRFQVKTGEVDYLAKE---LEVDNKKMGHVR 274
QY 122 FDLTLGNSLVTLCH-LENTHGLIHFKLDMTLHRLVWQEDYHSQNPYHNAVAHAD 180
DB 275 IABL-SGNRPILVIMHTIFQERDILKTFKIPVDLITYLMTLDDHYHADVAHNNINHAAD 333
QY 181 VTQAMHCYKEPKLASFLTPDLIMGLLAAAHADVHDHGVSNQPLITNNHNLANYOMNS 240
DB 334 VVOSTHVLSTPALDAVFTDLEILAIFASAHIDVDHGVSNQPLINTNSLALMTYDSS 393
QY 241 VLENHNRSTIGMLRESR--LLAHLPRKEMODIEOQLSILATDINRQNEFLTRLKAHL 298
DB 394 VLENHNLAVGFKLLQENHCDFQNLTKKQKQSLRKMYIDVLATDMSKHNMLADLKTWY 453
QY 299 HAKD-----LRLDAODRHFMQLIALKADICNPCRIMWSKQWSRVCEEFYRQGELE 352
DB 454 ETKKVTSSGVLLDNYSDRIQVLNNVHCADLSNPKRPLDLYRWQMDRIMEEFPQGDRE 513
QY 353 OKRELEISPLCNOQKDSIPSTIQIGFMSYIEPFLREVAHFTGNSLTSENMGLAHNAKAQ 412
DB 514 REGMETISPMCDKHNASVSKQVGFIDYIVHPLMETWADLVHPD--AQDILDTLEDNRKY 571
QY 413 KKSLEISPLCNRSGSGSPDHAG--QGTSE-----EQEGDS 449
DB 572 YQSTIPQ-----SPSPAPDDPEGRGQGTGKFOFELTLEDGES 610

RESULT 12
US-07-688-352C-4

;; Sequence 4, Application US/07688352C
;; Patent No. 5527896
;; GENERAL INFORMATION:
;; APPLICANT: Wiegler, Michael H.
;; APPLICANT: Colicelli, John J.
;; TITLE OF INVENTION: Cloning by Complementation and Related
;; TITLE OF INVENTION: Processes
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Bicknell
;; STREET: Two First National Plaza, 20 South Clark
;; STREET: Street
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60603
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/688,352C
;; FILING DATE: 19910419
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/511,715
;; FILING DATE: 20-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Borun, Michael F.
;; REGISTRATION NUMBER: 25447
;; REFERENCE/DOCKET NUMBER: 27805/30197
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 562 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-07-688-352C-4

Query Match 24.1%; Score 580.5; DB 1; Length 562;
Best Local Similarity 31.9%; Pred. No. 2.5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;
QY 66 KKKVKRLS---FQRYFNASRLRLGIIIPQAPRLHLLDEVDYLGQARHMLSKVGMWDDIFL 121
DB 124 KKKQOQMDTQISGVKKLMHSSSLNNTSISRFQVKTENEDHLAELEDLNK---WGLNTFN 180
QY 122 FDLTLGNSLVTLCHLFTNTHGLIHFKLDMTVLRFLVWQEDYHSQNPYHNAVAHADY 181
DB 181 VAGYSNRPILTCMAVIFQERDILKTFKISDFVYIYMTLEHHSYSDVAHYNSLAHADY 240
QY 182 TQAMHCYKEPKLASFLTPDLIMGLLAAAHADVHDHGVSNQPLITNNHNLANYOMNSY 241
DB 241 AOSTHVLSTPALDAVFTDLEILAIFAAAHIDVDHGVSNQPLINTNSLALMTYDESV 300
QY 242 LENHNRSTIGMLRESR--LLAHLPRKEMODIEOQLSILATDINRQNEFLTRLKAHL 299
DB 301 LENHNLAVGFKLLQENHCDFQNLTKKQKQSLRKMYIDVLATDMSKHNMLADLKTWY 360
QY 300 NKD-----LRLDAODRHFMQLIALKADICNPCRIMWSKQWSRVCEEFYRQGELE 353
DB 361 TKKVTSSGVLLDNYSDRIQVLNNVHCADLSNPKRPLDLYRWQMDRIMEEFPQGDKER 420
QY 354 KFELEISPLCNOQKDSIPSTIQIGFMSYIEPFLREVAHFTGNSLTSENMGLAHNAKAQ 413
DB 421 ERGMETISPMCDKHNASVSKQVGFIDYIVHPLMETWADLVQPD--AQDILDTLEDNRNMY 478

Oy 414 KSLPR-----QHRSGSSGSGPDHNDH-----AGGTSESEEGDSDP 450
Db 479 QSMIPQSPPLDERSRDCGLMEKFOFELTLEEDSEGEKRGEGP 525

RESULT 13

US-08-942-521B-8
Sequence 8, Application US/08942521B
Patent No. 5932477
GENERAL INFORMATION:
APPLICANT: Livi, George P.
APPLICANT: McLaughlin, Megan M.
APPLICANT: Torphy, Theodore J.
TITLE OF INVENTION: Human Brain Phosphodiesterase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Patents/P.O.Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,521B
FILING DATE: October 2, 1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/446,386
FILING DATE: 22 May 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,334
FILING DATE: 10 March 1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: 41,824
REFERENCE/DOCKET NUMBER: P50145CLFMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5009
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-942-521B-8

Query Match 24.1%; Score 580.5; DB 2; Length 562;
Best Local Similarity 31.9%; Pred. No. 2,5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

Oy 66 KKKYKRLS----FORFHASRLRGITIPQAPLHLDEEDYLGOARHMSKVGMMDDIFL 121
Db 124 KKKQQLMTQISGVKALMSSLNNTISIRGVNTEHEDHLAELEDLNL--WGLNTFN 180
Oy 122 FDRLTNGNSLVTLCILPNTGLIHNRKLDVTLHRELVNVOEDYNSONPYNAVAHADY 181
Db 181 VAGSYSHNRPLTCIMYALFOERDLTKTPKISSDFVYUMLLEDDHYSDVAYHNSLHAADY 240
Oy 182 TOAMHCYLKPKLASFLTPDLIMGLIAAAHNDVDPGVNQPPLIKTNHHLANLYOMMSV 241
Db 241 AOSTHVLSTPDLDAVETDELLAIAIFMAAIIHVDHFGVSNOPFLINTNSELLAMYNDES 300
Oy 242 LENHNRSTIGMLRESR--LLAHLPKEMTODIEQOLGSLILANDINRNEFLTRKANHD 299

Db 301 LENHHLAVGFKLLQEEHCDFONTKOROTLKRKVIDWLVATDMKSHMSLLADLKTWE 360
Oy 300 NKD-----LLEDAODRHFMLQIALKCADICNPCHRWMSKOWSERVCEEFYRGQLEQ 353
Db 361 TKKYTSSGVLLDDNYTDRIQVLRNMVHCADLSNPTKSLLEYRQWTDRIWEEFFQGDKER 420
Oy 354 KFELEISPLCNOCKDSIPSIQIGMSYVPLFREMAHFTGNSTSENNLGHILANKRAW 413
Db 421 ERGMEISPMCDKHRTASVEKSOVGFDIVLHPMETWADLVQPD--AQDILDFLEDRRMVY 478
Oy 414 KSLPR-----QHRSGSSGSGPDHNDH-----AGGTSESEEGDSDP 450
Db 479 QSMIPQSPPLDERSRDCGLMEKFOFELTLEEDSEGEKRGEGP 525

RESULT 14

US-08-474-379C-4
Sequence 4, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-4

Query Match 24.1%; Score 580.5; DB 2; Length 562;
Best Local Similarity 31.9%; Pred. No. 2,5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;
Oy 66 KKKYKRLS----FORFHASRLRGITIPQAPLHLDEEDYLGOARHMSKVGMMDDIFL 121

Db 124 KKKKQOLMTQISGVKKLMHSSSLNNTSISRFVNTENEDHLAKLEDLNK---WGLINFN 180
QY 122 FDLRTGNSLVTLCLFPTHGLIHFFKLDWTLNHRFLVWQVDYHSONPYNAVAADY 181
Db 181 VAGYSNRPILTCIMVAIFQERDLTKFKISSDTFTYMMTLDEHYSDVAYHNSLAAAY 240
QY 182 TQAMHCYLEPKLASEFLPLDLMGLLAAAHVDHDPGVNOPELITNHNLANLYONMSV 241
Db 241 AOSTHVLLSTPALDAVFTDEILAAIFAAAHVDHDPVSNQFLINTNSLALMYDESV 300
QY 242 LENHHNRSTIGMLRES--LLAHLPREMTODIEQUGSLILATDIRONEFLTRKAHLH 299
Db 301 LENHHLAVGEFKLQEHCHDFQMLTKRQOTLRKAVIDWVLAIDMSKHNSLADLKTWVE 360
QY 300 NKD-----LLEDAQDRHFMLOIALKCADICNCRIMWSKOWSRVCEEFYRQGELO 353
Db 361 TKKVTSSGVLLDNTDRIOVLNNVHCADLSNPTSLLEYKOWIDRIEERFQGDKER 420
QY 354 KELEISPLCNOQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSLSENNLGHLANHKAOW 413
Db 421 ERGMEISPMODKHTASVEKSQYGFIDYIYHPLMETWADLVQPD--AQDILDTLEDNRNY 478
QY 414 KSLLP-----QHSRSGSSGSPDDH---AGGTSESEBQEGDSP 450
Db 479 OSMIPQSPSPPLDERSRDCQGLMEKFOFELTLEEDSEGEPEKGESE 525

RESULT 15
US-09-146-249A-4
; Sequence 4, Application us/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-146-249A-4

Query Match

24.1%; Score 580.5; DB 3; Length 562;

Best Local Similarity 31.9%; Pred. No. 2,5e-52;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

QY 66 KKKVKLLS-----FQYFASRLRLRGITPOAPLHLIDDEYLGQARMLSKVGMDFDIL 121
Db 124 KKKKQOLMTQISGVKKLMHSSSLNNTSISRFVNTENEDHLAKLEDLNK---WGLINFN 180
QY 122 FDLRTGNSLVTLCLFPTHGLIHFFKLDWTLNHRFLVWQVDYHSONPYNAVAADY 181
Db 181 VAGYSNRPILTCIMVAIFQERDLTKFKISSDTFTYMMTLDEHYSDVAYHNSLAAAY 240
QY 182 TQAMHCYLEPKLASEFLPLDLMGLLAAAHVDHDPGVNOPELITNHNLANLYONMSV 241
Db 241 AOSTHVLLSTPALDAVFTDEILAAIFAAAHVDHDPVSNQFLINTNSLALMYDESV 300
QY 242 LENHHNRSTIGMLRES--LLAHLPREMTODIEQUGSLILATDIRONEFLTRKAHLH 299
Db 301 LENHHLAVGEFKLQEHCHDFQMLTKRQOTLRKAVIDWVLAIDMSKHNSLADLKTWVE 360
QY 300 NKD-----LLEDAQDRHFMLOIALKCADICNCRIMWSKOWSRVCEEFYRQGELO 353
Db 361 TKKVTSSGVLLDNTDRIOVLNNVHCADLSNPTSLLEYKOWIDRIEERFQGDKER 420
QY 354 KELEISPLCNOQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSLSENNLGHLANHKAOW 413
Db 421 ERGMEISPMODKHTASVEKSQYGFIDYIYHPLMETWADLVQPD--AQDILDTLEDNRNY 478
QY 414 KSLLP-----QHSRSGSSGSPDDH---AGGTSESEBQEGDSP 450
Db 479 OSMIPQSPSPPLDERSRDCQGLMEKFOFELTLEEDSEGEPEKGESE 525

Search completed: September 13, 2002, 12:05:51
Job time: 252 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 11:59:44 : Search time 31.9 Seconds
(without alignments)
1566.872 Million cell updates/sec

Title: US-09-471-459A-5

Perfect score: 2408

Sequence: 1 MSCLMVENCGEILFENPDQN.....PDHDAAGGTSEEGEGDSP 450

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/hold-genseq/genseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2408	100.0	450	21	AA93569	Amino acid sequenc
2	2408	100.0	450	22	AA678915	Human type 7B phos
3	2408	100.0	450	22	AAU08675	Human phosphodiester
4	2234	92.8	502	22	AA636503	Human long phospho
5	2219.5	92.2	451	21	AA93567	Amino acid sequenc
6	2192	90.0	446	21	AA93567	Amino acid sequenc
7	2165.5	89.9	445	21	AA93574	Amino acid sequenc
8	2165.5	89.9	445	21	AA93573	Amino acid sequenc
9	2121	88.1	437	21	AA93572	Amino acid sequenc
10	1990.5	82.7	413	21	AA93571	Amino acid sequenc
11	1865	77.5	391	22	AAU08676	Human phosphodiester

12	1430	59.4	268	21	AA93593	Amino acid sequenc
13	1430	59.4	288	21	AA93568	Amino acid sequenc
14	1419.5	58.9	498	17	AAU00094	CAMP phosphodiester
15	1419.5	58.9	498	20	AA49808	Human glioblastoma
16	1419.5	58.9	498	21	AA520619	PTM22 human gliobl
17	1286	53.2	432	22	AAU16967	Human novel secret
18	1280	53.2	320	22	AA636504	Human short phosph
19	771	32.0	211	22	AAU23004	Novel human enzyme
20	771	32.0	211	22	AAU18681	Renal and cardiora
21	771	32.0	211	22	AAU17039	Human novel secret
22	604.5	25.1	507	21	AA93995	Human novel secret
23	604.5	25.1	518	22	AA661185	Human PDE4d6 prote
24	604.5	25.1	673	20	AA49827	Human PDE4d6-like p
25	604.5	25.1	673	21	AA636538	pppE43 human dunce
26	604.5	25.1	673	21	AA93997	Amino acid sequenc
27	604.5	25.1	673	22	AA51411	Human phosphodiester
28	604.5	25.1	704	22	ABG06964	Novel human diagno
29	604.5	25.1	745	21	AA93996	Amino acid sequenc
30	604.5	25.1	929	22	AA65780	Amino acid sequenc
31	604.5	25.1	930	21	AA84876	Amino acid sequenc
32	604.5	25.1	1002	21	AA84878	Amino acid sequenc
33	604.5	25.1	1066	21	AA84877	Amino acid sequenc
34	603.5	25.1	517	22	AA661186	Rat PDE4d6 protein
35	599.5	24.9	674	17	AA69743	Human phosphodiester
36	598.5	24.9	1029	22	AA65779	Amino acid sequenc
37	580.5	24.1	562	12	AAU14836	"Dunce"-like phosph
38	580.5	24.1	562	17	AAU00090	Rat dunce-like pro
39	580.5	24.1	562	20	AA49803	Rat dunce-like pro
40	580.5	24.1	562	21	AA620614	Plasamid pRATPD 2.
41	580.5	24.1	564	22	AA604745	Rat CAMP-specific
42	580.5	24.1	659	22	AA604741	Rat CAMP-specific
43	580.5	24.1	721	22	AA604746	Rat CAMP-specific
44	580.5	24.1	736	22	AA604743	Rat CAMP-specific
45	567.5	23.6	564	15	AA60605	Brain low Km, CAMP

ALIGNMENTS

RESULT 1	
AA93569	standard; Protein; 450 AA.
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AC	AA93569;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a human phosphodiesterase enzyme.
XX	
KW	Phosphodiesterase; PDE-XIV; human; enzyme.
XX	
OS	Homo sapiens.
XX	
PN	EP1018559-A1.
XX	
PD	12-JUL-2000.
XX	
PF	09-NOV-1999; 99EP-0308902.
XX	
PR	23-DEC-1998; 98GB-0028603.
PR	17-SEP-1999; 99GB-0022123.
XX	
PA	(PFIZ) PFIZER LTD.
PA	(PFIZ) PFIZER INC.
PI	Ridock M;
XX	
DR	WPI; 2000-433274/38.
DR	N-PSDB; AAA46651.
XX	
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT	useful for preventing diagnosing and treating diseases associated with
PT	inappropriate PDE-XIV expression and/or activity -

XX Disclosure; Page 45-47; 104pp; English.

PS
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV agonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 21; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,3e-227;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCIWVRCGEILFENPDQNAKVCMLDILRGOTGVRAERKSGYFIDFLLNSTTYS 60
DB 1 mscIwvrcgeilfepdqnakvcmlgdilrgotgvraerksygidfllnsttys 60
QY 61 GEIGTKKKVKRLSFRFHFASRLRGIIPOAPRLHLEDEYLGQARHMLSKVGMDFDF 120
DB 61 geigtkkkvkrllsfrrfhfarsrlrgiipoarhlledeylgqarhmlskvgmddf 120
QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHHFKLDWVTLHRLFWVQEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnslvtlchlftnthglihhfkldwvtlhrflwvqedyhsqnpynavhad 180
QY 181 VTQAMHCYIKERKLASFETPLDMLGILAAAHVDHPVNOPELTKTNHNLANYQNS 240
DB 181 vtqamhcylkerklasfetipltldmlgilaaaahvdhpnvnopeltktnhnlanyqns 240
QY 241 VLENHHRSTIGMLRESRLAHLPRKEMTODIEQGLSLIATDINRONEFLTRKALHNLN 300
DB 241 vlenhhrstigmlesrlahlprkemtodieqglslilatdinronefltrkahlhnl 300
QY 301 KDLRLDAQDRHFMLOIALKCADICNPCRIMESKQWSRVCSEFEYRGQLEQFELEIS 360
DB 301 kdrlledaqdrhfmloialkcadicncprimeskqwsrvceefyrgqleqfeleis 360
QY 361 PLCNQKDSIPSIQIGFMSYIYEPFLREWAHFTGNTSLENMGLAHNAKQKSLPRQ 420
DB 361 plcnqkdsipsiqigfmsyiverflrewahftgntslennmglahnakqksllprq 420
QY 421 HRSRSGSGSPDHDHAGQGTSESEQGDSP 450
DB 421 hrsrsgsgspdhhdhagqgtseesegdsp 450

RESULT 2

AA078915
ID AAG78915 standard; protein; 450 AA.

XX AAG78915;

XX 19-DEC-2001 (first entry)

XX Human type 7B phosphodiesterase, PDE7B.

KW Human; type 7B phosphodiesterase; PDE7B; enzyme.

OS . Homo sapiens.

PN JP2001238680-A.

PD 04-SEP-2001.

PF 03-MAR-2000; 2000JP-0058159.

PR 03-MAR-2000; 2000JP-0058159.

PA (TANA) TANABE SEIYAKU CO.

DR WPI: 2001-610057/70.

DR N-PSDB: AA170009.

PS Claim 2; Page 12-14; 18pp; Japanese.

CC The present sequence is the protein sequence for human type 7B

CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the

CC development of inhibitors of high selectivity and drugs of low side

CC effects.

PS Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,3e-227;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCIWVRCGEILFENPDQNAKVCMLDILRGOTGVRAERKSGYFIDFLLNSTTYS 60
DB 1 mscIwvrcgeilfepdqnakvcmlgdilrgotgvraerksyfidfllnsttys 60
QY 61 GEIGTKKKVKRLSFRFHFASRLRGIIPOAPRLHLEDEYLGQARHMLSKVGMDFDF 120
DB 61 geigtkkkvkrllsfrrfhfarsrlrgiipoarhlledeylgqarhmlskvgmddf 120
QY 121 LFDRLTNGNSLVTLCHLFTNTHGLIHHFKLDWVTLHRLFWVQEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnslvtlchlftnthglihhfkldwvtlhrflwvqedyhsqnpynavhad 180
QY 181 VTQAMHCYIKERKLASFETPLDMLGILAAAHVDHPVNOPELTKTNHNLANYQNS 240
DB 181 vtqamhcylkerklasfetipltldmlgilaaaahvdhpnvnopeltktnhnlanyqns 240
QY 241 VLENHHRSTIGMLRESRLAHLPRKEMTODIEQGLSLIATDINRONEFLTRKALHNLN 300
DB 241 vlenhhrstigmlesrlahlprkemtodieqglslilatdinronefltrkahlhnl 300
QY 301 KDLRLDAQDRHFMLOIALKCADICNPCRIMESKQWSRVCSEFEYRGQLEQFELEIS 360
DB 301 kdrlledaqdrhfmloialkcadicncprimeskqwsrvceefyrgqleqfeleis 360
QY 361 PLCNQKDSIPSIQIGFMSYIYEPFLREWAHFTGNTSLENMGLAHNAKQKSLPRQ 420
DB 361 plcnqkdsipsiqigfmsyiverflrewahftgntslennmglahnakqksllprq 420
QY 421 HRSRSGSGSPDHDHAGQGTSESEQGDSP 450
DB 421 hrsrsgsgspdhhdhagqgtseesegdsp 450

RESULT 3

AA008675
ID AA008675 standard; protein; 450 AA.

XX AA008675;

DT 18-DEC-2001 (first entry)
XX
DE Human phosphodiesterase type 7B #1.
XX
KW Human; phosphodiesterase type 7B; cardiovascular disease;
KW asthma; allergy; inflammatory disease; immune-related disorder;
KW cardiovascular; antiallergic; antiallergic; immunosuppressive;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200162940-A2.
XX
PD 30-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-EP01858.
XX
PR 21-FEB-2000; 2000EP-0103655.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Kluxen F, Hentsch B;
XX
DR WPI: 2001-570636/64.
DR N-PSDB; AAS13248.
XX
PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
XX diagnosing and treating, e.g. asthma, inflammation and allergies -
PS Claim 1; Page 36-37; 40pp; English.
XX
XX The invention relates to a novel human phosphodiesterase type 7B
CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC acid may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC example, the protein and nucleic acid may be used to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of P7B by
CC expressing inactive proteins or to supplement the patients own
CC production of P7B. The nucleic acids may be used to produce P7B
CC polypeptides, by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The nucleic acid and its
CC complements may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The P7B
CC polypeptides may also be used as antigens in the production of
CC antibodies against P7B and in assays to identify modulators of it's
CC expression and activity. The anti-P7B antibodies and antagonists may
CC also be used to down regulate expression and activity. The anti-P7B
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Disorders that may be prevented, diagnosed and/or treated by
CC the above methods include, for example cardiovascular disease, asthma,
CC allergy, inflammation, and immune-related disorders. The present
CC sequence represents a human phosphodiesterase 7B.
XX
SQ Sequence 450 AA:

Query Match 100.0%; Score 2408; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.3e-22;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 lfdrltngslvtlclhlfntbgljnhfkldmvtclrlvmvgedyhsqpnynavhaad 180
QY 181 vtqamhcyllkepkrlasflrplrdlmgllaaadvyhrevnqpfllktnhlanlyqnm 240
DB 181 vtqamhcyllkepkrlasflrplrdlmgllaaadvyhrevnqpfllktnhlanlyqnm 240
QY 241 vlenhhwrstlcmrlresrlanhlprkemtodieqolstlilandynqneflrklahln 300
DB 241 vlenhhwrstlcmrlresrlanhlprkemtodieqolstlilandynqneflrklahln 300
QY 301 kdrlrleadaoqrhfmloialkacdicnprciwkskowservcebfyrgelbqefleis 360
DB 301 kdrlrleadaoqrhfmloialkacdicnprciwkskowservcebfyrgelbqefleis 360
QY 361 plcnqgkdsipsiqfymeylvepllrwahntgslsemlghlanhkaqkxllprq 420
DB 361 plcnqgkdsipsiqfymeylvepllrwahntgslsemlghlanhkaqkxllprq 420
QY 421 hrsrgssgsqpdhdhagocgteseeqgdsp 450
DB 421 hrsrgssgsqpdhdhagocgteseeqgdsp 450

RESULT 4
AAB36503
ID AAB36503 standard; Protein; 502 AA.
XX
AC AAB36503;
XX
DT 06-MAR-2001 (first entry)
XX
DE Human long phosphodiesterase protein SEQ ID NO.1.
XX
KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
KW cyclic nucleotide phosphodiesterase; nootropic; cardiant; hypotensive;
KW nephrotropic; antidepressant; antiinflammatory; immunosuppressive;
KW antifertility; antiallergic; vasotropic; gene therapy; dementia;
KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;
KW atopic disease; autoimmune encephalomyelitis; organ transplantation;
KW nephrotic syndrome; erectile dysfunction.
XX
OS Homo sapiens.
XX
PN US6146876-A.
XX
PD 14-NOV-2000.
XX
PF 11-JUN-1999; 99US-0330970.
XX
PR 26-MAR-1999; 99US-0277423.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, White D, Robison KE;
XX
DR WPI: 2001-023577/03.
DR N-PSDB; AAC87948.
XX
PT Polynucleotide encoding novel cyclic nucleotide phosphodiesterase
XX useful for treating disorders related with to protein e.g. dementia,
XX hypertension, glomerulonephritis, and organ transplantation -
PS Claim 3; Fig 1; 42pp; English.
XX
XX The present sequence represents the human long phosphodiesterase which
XX is a cyclic nucleotide phosphodiesterase (I). (I) can have nootropic,
XX cardiant, hypotensive, nephrotropic, antidepressant, antiinflammatory,
XX immunosuppressive, antifertility, antiallergic and vasotropic
XX activities, and can be used in gene therapy. (I) can be used for
XX treating various disorders associated or mediated by (I), such as
XX dementia, amnesia, congestive heart failure, thrombosis, pulmonary
XX hypertension, glomerulonephritis, bipolar depression, bronchial asthma,

CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,
 CC salt retention in nephrotic syndrome and erectile dysfunction.

XX Sequence 502 AA;

Query Match 92.8%; Score 2234; DB 22; Length 502;
 Best Local Similarity 99.1%; Pred. No. 3.1e-210;
 Matches 419; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 28 GDIRLRGOTGVRAERGSYPFDLRLNSTTSGEIGTKKKRRLSFQRYFNASRLRG 87
 Db 80 gdlrlrgygvraerrgsypfdlrlnsttsgelgkkrkrlsfqryfnasrlrg 139
 OY 88 IIPQAPLHLLDDYLGQARHMLSKVGMDFIPLFDRLTNGNSLVTLCHLFTNGHGIHH 147
 Db 140 iipqaplhllddylgqarhmlskvwmddfllfdrltngnslvtlchlfnhghlhh 199
 OY 148 EKIDAWTLHRELVMQEDYHSQNPYHNAVDYQAMHCYKRPKRLASPLTIDMLGL 207
 Db 200 fklidawtlhrelvmqedyhsqnpynaadvqamcykrepkrlaspltdmlgl 259
 OY 208 LAAAHADVDPVGNOPFLIKTNHLLANLYQNMSTVLENHNRSTIGMLRESRLAHLPEKM 267
 Db 260 laaahadvdpvgnopfliktnhllanlyqnmstvlenhnrstlglmlresrlahlpek 319
 OY 268 TDIDEOQSLTLATDINQNEFLTRKALHNLKDLRLDAQDRHMLQIALKCADI CNP 327
 Db 320 tdldeqsltlatdinonefltrkahlhnlkdlrledaqdrhmlqialkcadicnp 379
 OY 328 CRIEWSKQSERVCEEFYRQGLEQKPELEISPLCNOOKDSISIQIGMSYIVPELFR 387
 Db 380 criewskqserveefyrqgleqkpeleisplcnokdsipsiqgfmsyiveplfr 439
 OY 388 EWAHFTNSTLSENNLGHLANHKAQWKSILPROHRSRSGSGPDHMACGTSEEOEG 447
 Db 440 ewahftnsltsennlghlanhkaqkwlprhnrstrsgsgpdhmacgtseeseg 499
 OY 448 DSP 450
 Db 500 dsp 502

RESULT 5

AA93575
 ID AA93575 standard; Protein: 451 AA.

XX AA93575;

XX 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase: PDE-XIV; enzyme.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12 /label= Val, Ile

FT Misc-difference 16 /label= Ser, Asn

FT Misc-difference 18 /label= Glu, Asp

FT Misc-difference 20 /label= Ser, Val, Asn, Ala

FT Misc-difference 21 /label= Ser, Val, Asn, Ala

FT Misc-difference 30 /label= Val, Ile

FT Misc-difference 39 /label= Pro, Arg

FT Misc-difference 56

FT /label= Asn, Ser
 FT Misc-difference 59 /label= His, Tyr
 FT Misc-difference 114 /label= Thr, Met
 FT Misc-difference 141 /label= Ser, Thr
 FT Misc-difference 168 /label= Gly, His, Ser, Gln
 FT Misc-difference 169 /label= Gly, His, Ser, Gln
 FT Misc-difference 307 /label= Gly, His, Ser, Gln
 FT Misc-difference 308 /label= Asp, Ala, Asn, Val
 FT Misc-difference 350 /label= Asp, Ala, Asn, Val
 FT Misc-difference 379 /label= Glu, Asp
 FT Misc-difference 391 /label= Ser, Thr
 FT Misc-difference 391 /label= His, Arg
 FT Misc-difference 404 /label= Gly, Ser
 FT Misc-difference 418 /label= Pro, Arg, Ser, Asn
 FT Misc-difference 419 /label= Pro, Arg, Ser, Asn
 FT Misc-difference 423 /label= Ser, Arg
 FT Misc-difference 435 /label= His, Leu
 FT Misc-difference 438..440 /note= "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"
 FT Misc-difference 442..443 /note= "these residues are either Ser-Glu or Thr-Leu"
 FT Misc-difference 446 /note= "optionally absent"
 FT Misc-difference 449..450 /note= "these residues are either Asp-Ser or Ala-Thr"

EP1018559-A1.

PD 12-JUL-2000.

XX 09-NOV-1999; 99EP-0308902.

XX 23-DEC-1998; 98GB-0028603.

XX 17-SEP-1999; 99GB-0022123.

XX (PF12) PFIZER LTD.

XX (PF12) PFIZER INC.

XX Fidoack M;

XX WPI; 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity

XX Disclosure; Page 75-76; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

SQ Sequence 451 AA;

Query Match 92.2%; Score 2219.5; DB 21; Length 451;
Best Local Similarity 93.1%; Pred. No. 7.1e-209;
Matches 420; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 1 MSLAMERCEGELFENPDNAKVCVMIGDTRLGOTGVRAERGSYPFDIFRLNSTYTS 60
DB 1 mscImwercgevlfxepqxxkvcvcmgldvrltqgvgvaerqsyypfdifrlinstxs 60
QY 61 GEIGTKKKVRLSFQRYFHASRLRGIIPOAPLHLDEDEYLGQARHMLSKVGMDFDIF 120
DB 61 geigtkkkvrlsfqryfhassrlrgiipqaplhldedyisgarhmkskvgwdidf 120
QY 121 LFDRLTNGNSLVTLCHLFTNGLIHFKIDMYTLHREFLWVOEDYHSQNPYNAVAHAD 180
DB 121 lfdrltngnsylvtlchlftnshg1ihfkldmytlhrlwvgedy/hxnprynaavaad 180
QY 181 VTQAMHCYLKEPKLASFLPDLIMLGILAAADVDHDPGVNOPELRTKNHNLANKVONS 240
DB 181 vtqamhcylkepklaasflprldimlgilaaadvdhpyvngpfllktmhnlankvms 240
QY 241 VLENHHWRSTIGMLRESRLAHLPRKEMTODIEQOLSLIATDINRONEFLRLKAHLN 300
DB 241 vlenhhwrstigmresrlahlprkemtodieqolsliatdinroneflrlkahlhn 300
QY 301 KDLRLDADNRHMLQIALKADICNPCTRIWMSKQMSERVECEFFRQGLEBQFELEIS 360
DB 301 kdrlrlexqdrlhmlqialkadicnprtciwmskqmservceeffyrqgleqfelleis 360
QY 361 PLCNQOKDSTPSIQIGFMSYIVPELRFREMAHFTGNSLTSENMLGHANNAOKKSLPRQ 420
DB 361 plcnqokdstpsiqigfmyivepflrewarftgnstlsenmlghlanmkagwksllxxq 420
QY 421 HRSRGSSGSGPDHDHAGQGTSESEO-EGDSP 450
DB 421 hrsgsgsgpdhdhagqgtseseo 451

RESULT 6
AA93567
ID AA93567 standard; Protein; 446 AA.
XX
AC AA93567;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a murine phosphodiesterase enzyme.
XX
KM Phosphodiesterase; PDE-XIV; murine; enzyme.
XX
OS Mus sp.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PF 09-NOV-1999; 99EP-0308902.
XX

PR 23-DEC-1998; 98GB-0028603.
PR 17-SEP-1999; 99GB-0022123.

XX
XX (PF12) PFIZER LTD.
XX (PF12) PFIZER INC.

PI Fldock M;

DR WPI: 2000-433274/38.
N-PSDB: AAA46649.

PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity -

PS Disclosure; Page 39-41; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

SQ Sequence 446 AA;

Query Match 91.0%; Score 2192; DB 21; Length 446;
Best Local Similarity 91.6%; Pred. No. 3.5e-206;
Matches 413; Conservative 13; Mismatches 19; Indels 6; Gaps 2;

QY 1 MSLAMERCEGELFENPDNAKVCVMIGDTRLGOTGVRAERGSYPFDIFRLNSTYTS 60
DB 1 mscImwercgevlfxepqxxkvcvcmgldvrltqgvgvaerqsyypfdifrlinstxs 60
QY 61 GEIGTKKKVRLSFQRYFHASRLRGIIPOAPLHLDEDEYLGQARHMLSKVGMDFDIF 120
DB 61 geigtkkkvrlsfqryfhassrlrgiipqaplhldedyisgarhmkskvgwdidf 120
QY 121 LFDRLTNGNSLVTLCHLFTNGLIHFKIDMYTLHREFLWVOEDYHSQNPYNAVAHAD 180
DB 121 lfdrltngnsylvtlchlftnshg1ihfkldmytlhrlwvgedy/hxnprynaavaad 180
QY 181 VTQAMHCYLKEPKLASFLPDLIMLGILAAADVDHDPGVNOPELRTKNHNLANKVONS 240
DB 181 vtqamhcylkepklaasflprldimlgilaaadvdhpyvngpfllktmhnlankvms 240
QY 241 VLENHHWRSTIGMLRESRLAHLPRKEMTODIEQOLSLIATDINRONEFLRLKAHLN 300
DB 241 vlenhhwrstigmresrlahlprkemtodieqolsliatdinroneflrlkahlhn 300
QY 301 KDLRLDADNRHMLQIALKADICNPCTRIWMSKQMSERVECEFFRQGLEBQFELEIS 360
DB 301 kdrlrlexqdrlhmlqialkadicnprtciwmskqmservceeffyrqgleqfelleis 360
QY 361 PLCNQOKDSTPSIQIGFMSYIVPELRFREMAHFTGNSLTSENMLGHANNAOKKSLPRQ 420
DB 361 plcnqokdstpsiqigfmyivepflrewarftgnstlsenmlghlanmkagwksllsq 420
QY 421 HRSRGSSGSGPDHDHAGQGTSESEO-EGDSP 450

Db 421 hrrrgsg-----qdlagapapetleqtegatp 446

RESULT 7

AAV93574 ID AAV93574 standard; Protein; 446 AA.

XX AAV93574;

XX 25-SEP-2000 (first entry)

XX Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12 /label= Val, Ile

FT Misc-difference 16 /label= Ser, Asn

FT Misc-difference 18 /label= Glu, Asp

FT Misc-difference 20 /label= Ser, Val, Asn, Ala

FT Misc-difference 21 /label= Ser, Val, Asn, Ala

FT Misc-difference 30 /label= Val, Ile

FT Misc-difference 39 /label= Pro, Arg

FT Misc-difference 56 /label= Asn, Ser

FT Misc-difference 59 /label= His, Tyr

FT Misc-difference 114 /label= Thr, Met

FT Misc-difference 141 /label= Ser, Thr

FT Misc-difference 168 /label= Gly, His, Ser, Gln

FT Misc-difference 169 /label= Gly, His, Ser, Gln

FT Misc-difference 307 /label= Asp, Ala, Asn, Val

FT Misc-difference 308 /label= Asp, Ala, Asn, Val

FT Misc-difference 350 /label= Asp, Ala, Asn, Val

FT Misc-difference 379 /label= Glu, Asp

FT Misc-difference 391 /label= Ser, Thr

FT Misc-difference 404 /label= His, Arg

FT Misc-difference 418 /label= Gly, Ser

FT Misc-difference 419 /label= Pro, Arg, Ser, Asn

FT Misc-difference 423 /label= Pro, Arg, Ser, Asn

FT Misc-difference 430 /label= Ser, Arg

FT Misc-difference 433 /label= His, Leu

FT Misc-difference 434 /label= Gln, Gly, Thr, Pro, Ala

FT Misc-difference 435 /label= Gln, Gly, Thr, Pro, Ala

FT Misc-difference 437 /label= Ser, Glu, Thr, Leu

FT Misc-difference 438 /label= Ser, Glu, Thr, Leu
FT Misc-difference 441 /note= "optionally absent"
FT Misc-difference 444 /label= Asp, Ser, Ala, Thr
FT Misc-difference 445 /label= Asp, Ser, Ala, Thr
FT Misc-difference 445 /label= Asp, Ser, Ala, Thr

PN Ep1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PRIZ) PRIZER LTD.

XX (PRIZ) PRIZER INC.

XX Fidoack M:

XX WPI: 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
XX inappropriate PDE-XIV expression and/or activity -

XX Disclosure: Page 70-72; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
XX The enzyme sequence is derived from a formula of the invention. The
XX phosphodiesterase polynucleotide and polypeptide may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PDE-XIV expression. For example, the polynucleotide
XX be administered to treat diseases by rectifying mutations or deletions
XX in a patient's genome that affect the activity of PDE-XIV. They may
XX also be used to study the expression and function of PDE-XIV
XX polypeptides and their role in metabolism. The PDE-XIV polypeptides
XX may be used as antigens in the production of antibodies against PDE-XIV
XX and in assays to identify modulators (agonists and antagonists) of
XX PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
XX PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
XX and activity (i.e. the PDE-XIV gene and/or expression product may be
XX used in the preparation of a composition for the treatment of a disorder
XX associated with inappropriate PDE-XIV expression and/or activity and to
XX screen for agents that can modulate PDE-XIV expression and/or activity.
XX The anti-PDE-XIV antibodies may also be used as diagnostic agents for
XX detecting the presence of PDE-XIV polypeptides in samples (e.g. by
XX enzyme linked immunosorbant assay (ELISA)).

XX Sequence 446 AA;

Query Match 90.0%; Score 2166; DB 21; Length 446;
Best Local Similarity 91.6%; Pred. No. 1.2e-203;
Matches 413; Conservative 0; Mismatches 32; Indels 6; Gaps 2;

QY 1 MSLWVRCGEILFENPDONAKVCYMLGDIRLKGQGVRAERGSYPFDRLNSTYYS 60
DB 1 mslwvrcgeilfexpqxxkvcwmgdxrlrgqvgvxaerrgsypfdrlnstxts 60
QY 61 GEIGTKKKVKRLSFOREFHNSRLRGIIPQAPHLIDEDVYLGOARHMLSKGMDFDF 120
DB 61 geigtkkkvkrllsfqrfyfnasrlrlrglpgaphllldeedyjgqatlmkskgyxdldf 120
QY 121 LFDRLTNGNSIVTLTCHLFTNHGILHFRKLDWYTLRFLYVQVEDYHSQNPYHNAVHAD 180
DB 121 lfdrltngnsivtlclhlnfxhglilnhfkldawtclhrlfymvqedyhxsnpyhnavhaad 180
QY 181 VTQAMHCYLKPEKLASFETPLDIWGLLAADVDHDPGVNPFLLIKTNHHLANTYQNS 240
DB 181 vtqamhcykpeklasfletpldiwglaaadvdhdpgvnppflliktnhhlantyns 240

Query Match 89.9%; Score 2165.5; DB 21; Length 445;
 Best Local Similarity 91.3%; Pred. No. 1.4e-203;
 Matches 411; Conservative 1; Mismatches 33; Indels 5; Gaps 1;

QY 1 MSCIMVERGEILFENPDONAKCVMIGIRLGGTVNAERGSYPIDFRLNSTYVS 60
 1 mscimvergeexlfeexpqxxkvcvmlgdxlrqcyvaergrsyplfdfrllnxtxs 60
 Db 1 mscimvergeexlfeexpqxxkvcvmlgdxlrqcyvaergrsyplfdfrllnxtxs 60

QY 61 GEIGTKKKVRLSPQRYFENASRLRGITPOAPLNLDEDDYGGQAHMLSKVGMWDPDIF 120
 61 geigtkkkvrrllsfgyfhasrrllrgilrpqarhlldedyggqarhmlskvqwdfdif 120
 Db 61 geigtkkkvrrllsfgyfhasrrllrgilrpqarhlldedyggqarhmlskvqwdfdif 120

QY 121 LFDRLTGNLSLVTLLCHLFTNGLINHFKLDWYTLRFVWVQGEYHSQNPYHNAVHAD 180
 121 lfdrltngnslvtllchlfntnqlinhfkldwylhrflvmvqedyhxknpynhavad 180
 Db 121 lfdrltngnslvtllchlfntnqlinhfkldwylhrflvmvqedyhxknpynhavad 180

QY 181 VTOAMHGYLKEPKIASFLPRLDIMGLLAAAHNDVDHGVNQRPILIKNNHIANXQMS 240
 181 vtoamhgyllkepkiasflrpldimgllaaaahndvdhgvnqrpiliktannianxqms 240
 Db 181 vtoamhgyllkepkiasflrpldimgllaaaahndvdhgvnqrpiliktannianxqms 240

QY 241 VLENHNRSTIGMLRESRLIHLPRKMTODIEQGLSLTLDVIRKQNEFLTRKALHLN 300
 241 vlenhnrstlglmresrliahlpkemtqdieqgl9sl1laldlnrqnelfrlkahlhn 300
 Db 241 vlenhnrstlglmresrliahlpkemtqdieqgl9sl1laldlnrqnelfrlkahlhn 300

QY 301 KDLRLDADNRHMLDIALKCADICNPRIWKSQMSRVCSEFYRQGELEQKFELEIS 360
 301 kdrlldadnrhmlodialkcadicnpriwksqmsrvcseefyrgxlqkfeleis 360
 Db 301 kdrlldadnrhmlodialkcadicnpriwksqmsrvcseefyrgxlqkfeleis 360

QY 361 PLNQOKDSIPSIQIGFMSYIVELPRFEMAHFTGNSTLSENNLGHLANHKQWKSLLPRQ 420
 361 plncqgkdsipsiqigfmsyiveprfemahftgnstlsennlghlanhkqkwksllxqg 420
 Db 361 plncqgkdsipsiqigfmsyiveprfemahftgnstlsennlghlanhkqkwksllxqg 420

QY 421 HRSRGSQSGPDDHAGQTESEEGDSDP 450
 421 hrxrgrsx----xdkagxxexxegtegrxxp 445
 Db 421 hrxrgrsx----xdkagxxexxegtegrxxp 445

RESULT 9
 AAY93572
 ID AAY93572 standard; Protein; 437 AA.
 AC AAY93572;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of a phosphodiesterase enzyme.
 XX
 KW phosphodiesterase; PDE-XIV; enzyme.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH MISC-difference 12 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 16 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 18 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 20 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 29 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 29 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 38 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 38 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 53 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 58 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 113 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 140 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 167 /note= "any suitable peptide sequence or amino acid"

FT /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 305 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 347 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 376 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 388 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 401 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 415 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 419 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 423 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 425 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 428 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 430 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 433 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 436 /note= "any suitable peptide sequence or amino acid"
 FT MISC-difference 436 /note= "any suitable peptide sequence or amino acid"
 FT EP108559-A1.
 PN 12-JUL-2000.
 PD
 XX
 PF 09-NOV-1999; 99EP-0308902.
 PR 23-DEC-1998; 98GB-0028603.
 PR 17-SEP-1999; 99GB-0022123.
 XX
 PA (Pfizer) Pfizer Ltd.
 PA (Pfizer) Pfizer Inc.
 PI
 PI Fldock M;
 XX
 DR WPI; 2000-433274/38.
 XX
 PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
 PT useful for preventing diagnosing and treating diseases associated with
 PT inappropriate PDE-XIV expression and/or activity -
 XX
 PS Disclosure; Page 58-60; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
 CC The enzyme sequence is derived from a formula of the invention. The
 CC phosphodiesterase polynucleotide and polypeptide may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PDE-XIV expression. For example, the polynucleotide
 CC be administered to treat diseases by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of PDE-XIV. They may
 CC also be used to study the expression and function of PDE-XIV
 CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
 CC may be used as antigens in the production of antibodies against PDE-XIV
 CC and in assays to identify modulators (agonists and antagonists) of
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
 CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
 CC and activity (i.e. the PDE-XIV gene and/or expression product may be
 CC used in the preparation of a composition for the treatment of a disorder
 CC associated with inappropriate PDE-XIV expression and/or activity and to
 CC screen for agents that can modulate PDE-XIV expression and/or activity.
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
 CC enzyme linked immunosorbant assay (ELISA)).
 CC
 XX Sequence 437 AA;

KW	asthma; allergy; inflammatory disease; immune-related disorder;
KV	cardiovascular; antiasthmatic; antiallergic; immunosuppressive;
XV	antiinflammatory.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 188 /note= "Encoded by GAR"
FT	Misc-difference 188 /label= Unknown
FT	/note= "Encoded by CMC"
FT	Misc-difference 387
FT	/label= Unknown
FX	/note= "Encoded by GNN"
PN	WO200162940-A2.
PD	30-AUG-2001.
XX	
PF	20-FEB-2001; 2001WO-EP01858.
PR	21-FEB-2000; 2000EP-0103655.
XX	
PA	(MERE) MERCK PATENT GMBH.
PI	Kluxen F, Hentsch B;
DR	WPt: 2001-570636/64.
N-PSDB:	AAS13249.
PT	Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
XX	diagnosing and treating, e.g. asthma, inflammation and allergies -
XX	
PS	Claim 1; Page 39-40; 40pp: English.
XX	
CC	The invention relates to a novel human Phosphodiesterase type 7B
CC	polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC	acid may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC	example, The protein and nucleic acid may be used to treat
CC	disorders associated with decreased expression by rectifying mutations
CC	or deletions in a patient's genome that affect the activity of P7B by
CC	* expressing inactive proteins or to supplement the patients' own
CC	production of P7B. The nucleic acids may be used to produce P7B
CC	polypeptides, by inserting the nucleic acids into a host cell and
CC	culturing the cell to express the protein. The nucleic acid and its
CC	complementing may also be used as DNA probes in diagnostic assays to detect
CC	and quantitate the presence of similar nucleic acids in samples, and
CC	therefore which patients may be in need of restorative therapy. The P7B
CC	polypeptides may also be used as antigens in the production of it's
CC	antibodies against P7B and in assays to identify modulators of it's
CC	expression and activity. The anti-P7B antibodies and antagonists may
CC	also be used to down regulate expression and activity. The anti-P7B
CC	antibodies may also be used as diagnostic agents for detecting the
CC	presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
CC	(ELISA)). Disorders that may be prevented, diagnosed and/or treated by
CC	the above methods include, for example cardiovascular disease, asthma,
CC	allergy, inflammation, and immune-related disorders. The present
CC	sequence represents a human phosphodiesterase 7B.
XX	
Sequence	391 AA:

[illegible]

Db	70	uvmgdffdfldfrldnpgnslvcllchldfntrgldldhnhkldamtyldhldflvmxygedyhaspr	129
Oy	172	YHNNVNAADTOMAGNYUJKEPRLASFLPRDYMIGLLAAADNVDPYRGONORFLIKTPNNH	231
Db	130	yhaavhadvtqvmhcykxeprlasflfrldldmglldaaahdvbrpynqpfllkxnh	189
Oy	232	LANLYOMSVYLENNHNRKSTIGLAKESRYLAAHLPKEMTOROLOSLIADIPKONEFL	291
Db	190	lanlyomsvylenhvstfslgmldresrlaldrkremtqgdqgslldadlnpynefl	249
Oy	292	TRLKANIHNNDYLEDAORNYRMYLOIALKADJCNDPCRLIEMSKQWSEVCEEFROGEL	351
Db	250	trlkahlhkhkdrldleaqdgrthmglakscadlnoprxlwmkscqwsveeefyrgel	309
Oy	352	EOKFKELEISPLCNOOKDSTPRLTGTGFMYSUYEPLFRFMAHFGNSTLSBNMLIGHANPKA	411
Db	310	eqkfglelslpmlcpgkdxlpsrldqgfmusyalepablmahfegnstlqtcswatfahnkq	369
Oy	412	QWKSLLPRQHRKSGSGSGSGSRPH	433
Db	370	qwkxllpsrteagaaalaxghldh	391

RESULT	12
ID	AAV93593
XX	AAV93593 standard; Protein; 268 AA.
AC	
XX	AAV93593:
DT	25-SEP-2000 (first entry)
DE	Amino acid sequence of a human phosphodiesterase enzyme.
XX	
KW	Phosphodiesterase; PDE-XIV, enzyme.
OS	Homo sapiens.
XX	
PN	EPI018559-A1.
PD	12-JUL-2000.
PE	09-NOV-1999; 99EP-0308902.
XX	
DR	23-DEC-1998; 98GB-0028603.
PR	17-SEP-1999; 99GB-0022123.
XX	
PA	(PFI2) PFIZER LTD.
PL	(PFI2) PFIZER INC.
F1	
FL	Fidock M;
DR	WPI: 2000-433274/38.
XX	
FT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
FT	useful for preventing diagnosing and treating diseases associated with
FT	Inappropriate PDE-XIV expression and/or activity -
XX	
PS	Disclosure: Page 87-88; 104pp; English.
CC	
CC	The present sequence represents a phosphodiesterase (PDE) enzyme. The
CC	phosphodiesterase polynucleotide and polypeptide may be used in the
CC	prevention, treatment and diagnosis of diseases associated with
CC	Inappropriate PDE-XIV expression. For example, the polynucleotide
CC	be administered to treat diseases by rectifying mutations or deletions
CC	in a patient's genome that affect the activity of PDE-XIV. They may
CC	also be used to study the expression and function of PDE-XIV
CC	polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC	may be used as antigens in the production of antibodies against PDE-XIV
CC	and in assays to identify modulators (agonists and antagonists) of
CC	PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC	PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC	and activity (i.e. the PDE-XIV gene and/or expression product may be

CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 268 AA;

Query Match 59.4%; Score 1430; DB 21; Length 268;
Best Local Similarity 100.0%; Pred. No. 9.3e-132;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCLWRECGEILFENPDQNAKVCMLGDIRLRSRGTVRAERGSYPFIDRLNSTYS 60
DB 1 mscLwreGellfEnpdqnaKvcmlgDirlrsgTvraerGsypfIdrlnStys 60
QY 61 GEIGTKKKVKRLSFQRYFHASRLRGIIPOAPLHLDEDDYLGOAHMLSKVGMPDFDI 120
DB 61 geIgTkKkVkrLsfQryfHaSrllrgIiPqApLhlDeDyLgqArHmLSkvgMdfDI 120
QY 121 LFDRLNGNSLVTLCHLENTGHLHFKIDWTLHRLVWQEDYHSQNPYHNAVHAAD 180
DB 121 lFdrlNgnsLvTlChLEntGhLhFkIdWtLhRlVwQeDyHsqNpyHnaVhaad 180
QY 181 VTQAMHCYKLEPKLASFLPDIIMGLLAAAHVDHPGVNOPELTKTNHHLANLYQNS 240
DB 181 vtqAmHcYlEpKlAsfLpIdImIglLaaahVdHPgvNoPElTKtNHHLanLyqNs 240
QY 241 VLENHMRSTIGMLRESRLAHLPKEMT 268
DB 241 vlenHmrStIgmlrEsrlahlpkEmt 268

RESULT 13

AAV93568
ID AAV93568 standard; Protein; 288 AA.

AC AAV93568;

DT 25-SEP-2000 (first entry)

XX Amino acid sequence of a human phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; human; enzyme.

XX Homo sapiens.

XX EP1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

PI Fidoock M;

DR WPI: 2000-433274/38.

DR N-PSDB; AAA46650.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
XX inappropriate PDE-XIV expression and/or activity -

PS Disclosure: Page 42-44; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The

CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e., the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 288 AA;

Query Match 59.4%; Score 1430; DB 21; Length 288;
Best Local Similarity 100.0%; Pred. No. 1e-131;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCLWRECGEILFENPDQNAKVCMLGDIRLRSRGTVRAERGSYPFIDRLNSTYS 60
DB 1 mscLwreGellfEnpdqnaKvcmlgDirlrsgTvraerGsypfIdrlnStys 60
QY 61 GEIGTKKKVKRLSFQRYFHASRLRGIIPOAPLHLDEDDYLGOAHMLSKVGMPDFDI 120
DB 61 geIgTkKkVkrLsfQryfHaSrllrgIiPqApLhlDeDyLgqArHmLSkvgMdfDI 120
QY 121 LFDRLNGNSLVTLCHLENTGHLHFKIDWTLHRLVWQEDYHSQNPYHNAVHAAD 180
DB 121 lFdrlNgnsLvTlChLEntGhLhFkIdWtLhRlVwQeDyHsqNpyHnaVhaad 180
QY 181 VTQAMHCYKLEPKLASFLPDIIMGLLAAAHVDHPGVNOPELTKTNHHLANLYQNS 240
DB 181 vtqAmHcYlEpKlAsfLpIdImIglLaaahVdHPgvNoPElTKtNHHLanLyqNs 240
QY 241 VLENHMRSTIGMLRESRLAHLPKEMT 268
DB 241 vlenHmrStIgmlrEsrlahlpkEmt 268

RESULT 14

AAW00094
ID AAW00094 standard; Protein; 498 AA.

AC AAW00094;

DT 09-OCT-1996 (first entry)

XX CAMP phosphodiesterase encoded by plasmid PTM22 (ATCC 68601).

XX Human: glioblastoma cell; heat shock sensitivity; phosphodiesterase;
XX deficient yeast strain 10DB; PTM22; rat DpD phosphodiesterase; pde1-;
XX bovine Ca2+/calmodulin dependent CAMP phosphodiesterase; heart; plasmid;
XX RAS2(val19); pde2-; PTM3; PTM72; PRATPD; pUC99; rolipram sensitive.

XX Homo sapiens.

XX US5527896-A.

PN 18-JUN-1996.

PD 20-APR-1990; 90US-0511715.

PF 19-APR-1991; 91US-0688352.

PR 20-APR-1990; 90US-0511715.

XX

PA (COLD-) COLD SPRING HARBOR LAB.
XX Colicelli JT, Wigler MH;
XX WPI: 1996-299902/30.
DR N-PSDB; AAT34376.
XX

PI DNA mols. isolated from human glioblastoma cells - encode
XX RAS-related or cyclic nucleotide phosphodiesterase proteins
XX

PS Claim 4; Column 67-70; 101pp; English.

CC The sequences given in AAM0092-94 are encoded by plasmid fragments
CC which contain human glioblastoma cell cDNA inserts which are capable of
CC correcting the heat shock sensitivity of the phosphodiesterase
CC deficient yeast strain 10DAB. Several cDNA's were isolated and
CC sequenced. pTM22 encodes a novel human gene. From computer analysis,
CC pTM22 putatively encodes a protein homologous to various CAMP
CC phosphodiesterases, such as the bovine Ca2+/calmodulin dependent CAMP
CC phosphodiesterase and the rat DPD phosphodiesterase. Sequences related
CC to pTM22 were found to be expressed in human heart. Plasmid pTM22 was
CC unable to correct the heat shock sensitivity of RAS2(vall19) yeast
CC strains. It thus appears that the pde1- and pde2- yeast strain 10DAB
CC is more sensitive to phenotypic reversion by mammalian CAMP
CC phosphodiesterase clones than is the RAS2(vall19) yeast strain. The
CC inserts in the plasmids pTM3 and pTM72 were also characterized. These
CC two different CAMP phosphodiesterase cDNA's were found to be closely
CC related to, but distinct from, the PRATDP insert and the pC99 insert.
CC Biochemical analysis of cell lysates has established that the cDNA's of
CC pTM3 and pTM72, pJC44x and PRATDP encode rolipram sensitive CAMP
CC phosphodiesterases.
XX

Sequence 498 AA;

Query Match 58.9%; Score 1419.5; DB 17; Length 498;
Best Local Similarity 61.7%; Pred. No. 2.5e-130;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

OY 7 ERCEGTELENDPDKAKVCMLGDIRLKGOTGVAERRGSPYFDIFRLNSTYSGEIGTK 66
DB 62 qrrgalysdsdqatalymldgdyrvrsrgfseerrgsyprydfifhsqselewsa 121
OY 67 KKVKKLLSFQRYFNASRLGIIPOAPYLHLDDEYLGQARNHLSKVGMDFIFLDRLT 126
DB 122 mlrrllsfqylrsstfrfgtavsnsllldddnggakmlekvgnmfdlfdlft 181
OY 127 NGNSLVTLCHLENTFNGLIHNFKLDWVTLHRFLVWQEDYHSQNPYHNAVHADVTQAMH 186
DB 182 ngnslvstlchlentfnglihnfklwvltlhrflvwmqedyhsqnpynhavhadvtqamh 241
OY 187 CYLKEPKLASFLRPLDMLGLAAAHADVDHPCVNOPFLIKTNHNLANLYOMSVLENNH 246
DB 242 cylkepklasflrpldlmglaaaahadvhpcvnopflfikttnhnlanylomsvlennh 301
OY 247 WRSTGMLRESRLANPKREMTODIEQGLSLFLATDIRONPFLTRKKAHLNHNDRLE 306
DB 302 wrsagvllresgflshplreslqmetqgalllatdlsrgeylsflshdtrdgle 361
OY 307 DAOORHMLQALKCADICPCRIEMSKOMSRVCEFFYRGLEFQKFELEISPCMOQ 366
DB 362 dtrhrhylvlqalkcadicpcrtwelskqsekveeffngldlekynhlgvspldcrh 421
OY 367 KDSIPSTQIGFMSTYVERFERNAHFTGNSLSENMGLHLANKKQMSLLPRQHRSGS 426
DB 422 testaanqigfmstyerfernahftgnslsenmglhlankkqmsllprqhrsgh 480
OY 427 SGS 429
DB 481 daa 483

RESULT 15

AA49808
ID AA49808 standard; Protein: 498 AA.
XX

AC AA49808;
XX
XX 19-JAN-2000 (first entry)
DT
DE Human glioblastoma cell CAMP phosphodiesterase pTM22 protein.

XX Phosphodiesterase; dunce-like phosphodiesterase; pDE; DPD; CAMP;
XX RAS-related protein; immunoreactive; detection; genetic defect;
XX bronchodilation; increased myocardial contractility;
XX anti-inflammation.
XX

OS Homo sapiens.

PN US5977305-A.

XX 02-NOV-1999.

XX 07-JUN-1995; 95US-0474379.

XX 01-MAR-1994; 94US-0206188.

XX 20-APR-1990; 90US-0511715.

XX 19-APR-1991; 91US-0688352.

PA (COLD-) COLD SPRING HARBOR LAB.

PI Colicelli JT, Wigler MH;

XX WPI: 1996-619709/73.

XX N-PSDB; AA32240.

PT New isolated RAS-related polypeptides and mammalian cyclic nucleotide
PT phosphodiesterases, used for screening for agents which can modify
PT complement or suppress genetic defects -
XX

PS Claim 2; Column 85-88; 145pp; English.

CC The present invention describes new isolated RAS-related polypeptides
CC and mammalian cyclic nucleotide phosphodiesterases (pDES). RAS-related
CC polypeptides are capable of complementing a defective RAS function in
CC yeast. The products can be used for screening for agents which can
CC modify, complement or suppress a genetic defect in a biochemical
CC pathway in which CAMP participates, or in a biochemical pathway which
CC is controlled, directly or indirectly, by a RAS protein and other
CC proteins affecting cell growth and maintenance. Developing agents that
CC will selectively act upon pDES is directed toward reproducing the
CC desirable effects of cyclic nucleotides, e.g. bronchodilation,
CC increased myocardial contractility, anti-inflammation, yet without
CC causing the undesirable effects, e.g. increased heart rate or enhanced
CC lipolysis. The products can also be used for therapeutic, diagnostic
CC and prognostic uses. AA32229 to AA32285, and AA49803 to AA49830,
CC represent sequences used in the exemplification of the present
CC invention.
XX

Sequence 498 AA;

Query Match 58.9%; Score 1419.5; DB 20; Length 498;
Best Local Similarity 61.7%; Pred. No. 2.5e-130;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

OY 7 ERCEGTELENDPDKAKVCMLGDIRLKGOTGVAERRGSPYFDIFRLNSTYSGEIGTK 66
DB 62 qrrgalysdsdqatalymldgdyrvrsrgfseerrgsyprydfifhsqselewsa 121
OY 67 KKVKKLLSFQRYFNASRLGIIPOAPYLHLDDEYLGQARNHLSKVGMDFIFLDRLT 126
DB 122 mlrrllsfqylrsstfrfgtavsnsllldddnggakmlekvgnmfdlfdlft 181
OY 127 NGNSLVTLCHLENTFNGLIHNFKLDWVTLHRFLVWQEDYHSQNPYHNAVHADVTQAMH 186

Db 182 ngnslvsltfhlsfshgllfeyfhlldmmlrrflvmiqedyhsqnpynhavhaadvlqamh 241
 QY 187 CYKEPKRIASFLPLDIMGILAAAHADVDHPCVNOPFLIKTNHHLANLYQNMSTVLNNH 246
 Db 242 cyikepkriansvcpwdllslaaatndidhpgvnpfltktnhylatllykntsvlenhh 301
 QY 247 WRSTIGMLRESRLAHLPKEMTODIEQOLSLIATDINRONEFLTRLKAHLNKKDLRL 306
 Db 302 wrsavglresglsfshplesrqqmetqigalllatdlsrqneylsfshldrgdicle 361
 QY 307 DAODRPFMIQIALKCADICNPKRIMENSKOMSERVCEEFYRQGELEOKFELEISPLCNOQ 366
 Db 362 dtrhrhlvqmalckadlcpcrtwelsskqwksekteeffhgqglekkyhlyvspldcrh 421
 QY 367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMIGHLAHNKAOWKSILPROHRSRGS 426
 Db 422 tesianigqgfmtylveplftewarfs-ntrlsqtmghvglnkaawkgllqregssedt 480
 QY 427 SGS 429
 Db 481 daa 483

Search completed: September 13, 2002, 12:05:28
 Job time: 344 sec

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Db 61 IPQAPLHDEDEYLGQARHMLSKVGMDDLTLEPRLNNGSLVTLCHLHNTGLHNF 120
QY 149 KLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMHCYIKERKLASFPLDMLGL 208
Db 121 KLMVTLHRLVWVQEDYHSQNPYHNAVADVTQAMCYIKERKLASFPLDMLGL 180
QY 209 AAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENHNRSTIGMLRESRLAHLPKEMT 268
Db 181 AAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENHNRSTIGMLRESRLAHLPKEMT 240
QY 269 QDIEQOGLSLATDINRONEFELTRKALHNRKDLRLDADDRHFMQLKALCADIQNC 328
Db 241 QDIEQOGLSLATDINRONEFELTRKALHNRKDLRLDADDRHFMQLKALCADIQNC 300
QY 329 RIMEMSKOMSERVCEEFYRQGELEQKFELEISPLCNOQKDSIPSIQGFMSYIEPLFRE 388
Db 301 RIMEMSKOMSERVCEEFYRQGELEQKFELEISPLCNOQKDSIPSIQGFMSYIEPLFRE 360
QY 389 WAHFTGNTSENMGLHNLANKAOMKSLPROMRSRSGSGSPDHADAGOSTESEBQED 448
Db 361 WAHFTGNTSENMGLHNLANKAOMKSLPROMRSRSGSGSPDHADAGOSTESEBQED 420
QY 449 SP 450
Db 421 SP 422
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RESULT 2
QYERB3 PRELIMINARY: PRT: 482 AA.
ID QYERB3;
AC Q96R72;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CAMP PHOSPHODIESTERASE 7A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RX EMBL: AY007702; AAG16295.1;
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN, TESTIS;
RX MEDLINE=20483661; Pubmed=11027622;
RA Wang P., Wu P., Egan R.M., Billah M.M.;
RT Cloning, Characterization, and Tissue Distribution of Mouse
RT Phosphodiesterase 7A1.
RL Biochem. Biophys. Res. Commun. 276:1271-1277(2000).
DR EMBL: AY007702; AAG16295.1;
DR InterPro: IPR003607; HDC.
DR Pfam: PFO0233; PDase.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00471; HDC.
DR PROSITE: PS00126; PDASE_1; UNKNOWN.1.
SQ SEQUENCE 482 AA; 55288 MW; E8470DD85BFF7714 CRC64;
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Query Match 59.3%; Score 1427.5; DB 11; Length 482;
Best Local Similarity 62.2%; Pred. No. 14e-117;
Matches 263; Conservative 72; Mismatches 87; Indels 1; Gaps 1;

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QY 7 ERGCEILFENPDONAKVCMLGDRLRGQTVGAERKSYPIIDRLINSTYSGEIGTK 66
Db 46 QRGALSYDSDDOTALYIRMLGDVRYRSGAEGESERKSHYIDRIFHSOSEIEVSVA 105
QY 67 KVKRLLSFQRYFFHARLLRGLIIPQAPLHDEDEYLGQARHMLSKVGMDDLTLEPRL 126
Db 106 RNIIRLLSFQRYRKRSSRGATVCSLDIIDEYNGQAKMLKRVGNWMDIFLFDRLT 165
QY 127 NGNSLVTLCHLHNTGLHNFKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 186
Db 166 NGNSLVTLHFLHSLHGLIEFHLDMVKLRFLVMIQEDYHSQNPYHNAVADVTQAMH 225
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QY 187 CYLKEPKLASFLPPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 246
Db 226 CYLKEPKLASSVPWPDMLLSLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 285
QY 247 WRSTIGMLRESRLAHLPKEMTQDIEQOGLSLATDINRONEFELTRKALHNRKDLRL 306
Db 286 WRSVAGLLRESGLFSHLPLESRQMEAOIGALITATDISRONEYLSLFRSHLDGDL 345
QY 307 DAOHRHFMQLKALCADIQNCPRIMEMSKOMSERVCEEFYRQGELEQKFELEISPLCNOQ 366
Db 346 DGRHRHVLQWALKACADIQNCPRNMELSKOMSEKYTEFFHQGDIEKKYHLGVSPLCDRQ 405
QY 367 KDSIPSIQGFMSYIEPLFREWAHFTGNTSENMGLHNLANKAOMKSLPROMRSRGS 426
Db 406 TESTIANIQGFMTYLVLEPFLTEWARS-DTRLSQTMLGHVGLNKSATWGLQROQPSSEDA 464
QY 427 SGS 429
Db 465 NAA 467
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RESULT 3
QY6772 PRELIMINARY: PRT: 424 AA.
ID QY6772;
AC Q96T72;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CAMP-SPECIFIC CYCLIC NUCLEOTIDE PHOSPHODIESTERASE PDE7A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RX EMBL: AF32652; AAK57640.1;
RP SEQUENCE FROM N.A.
RC MEDLINE=21265467; Pubmed=11371644;
RA Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;
RT "T cell activation up-regulates cyclic nucleotide phosphodiesterases
RT 8A1 and 7A3."
RL Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).
DR EMBL: AF32652; AAK57640.1;
SQ SEQUENCE 424 AA; 48827 MW; A7DBF40D08A7B561 CRC64;
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Query Match 53.4%; Score 1287; DB 4; Length 424;
Best Local Similarity 62.7%; Pred. No. 2.9e-105;
Matches 235; Conservative 64; Mismatches 76; Indels 0; Gaps 0;

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QY 7 ERGCEILFENPDONAKVCMLGDRLRGQTVGAERKSYPIIDRLINSTYSGEIGTK 66
Db 46 QRGALSYDSDDOTALYIRMLGDVRYRSGAEGESERKSHYIDRIFHSOSEIEVSVA 105
QY 67 KVKRLLSFQRYFFHARLLRGLIIPQAPLHDEDEYLGQARHMLSKVGMDDLTLEPRL 126
Db 106 RNIIRLLSFQRYRKRSSRGATVCSLDIIDEYNGQAKMLKRVGNWMDIFLFDRLT 165
QY 127 NGNSLVTLCHLHNTGLHNFKLDVTLHRLVWVQEDYHSQNPYHNAVADVTQAMH 186
Db 166 NGNSLVTLHFLHSLHGLIEFHLDMVKLRFLVMIQEDYHSQNPYHNAVADVTQAMH 225
QY 187 CYLKEPKLASFLPPLDMLGLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 246
Db 226 CYLKEPKLASSVPWPDMLLSLAAAHVDHGVNQPFLIKTNHNLANTYONMSVLENH 285
QY 247 WRSTIGMLRESRLAHLPKEMTQDIEQOGLSLATDINRONEFELTRKALHNRKDLRL 306
Db 286 WRSVAGLLRESGLFSHLPLESRQMEAOIGALITATDISRONEYLSLFRSHLDGDL 345
QY 307 DAOHRHFMQLKALCADIQNCPRIMEMSKOMSERVCEEFYRQGELEQKFELEISPLCNOQ 366
Db 346 DTRHRHVLQWALKACADIQNCPRCTWELSKOMSEKYTEEFFHQGDIEKKYHLGVSPLCDRH 405
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DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE SIMILAR TO PHOSPHODIESTERASE 4B, CAMP-SPECIFIC (DUNNE
 DE (DROSOPHILA)-HOMOLOG PHOSPHODIESTERASE E4) (FRAGMENT).
 OS Mus musculus (mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007155; AAH07155.1; -
 FT NON_TER 1 1
 SQ SEQUENCE 542 AA; 62279 MW; 8B6296DA16275B34 CRC64;

Query Match 23.8%; Score 573.5; DB 11; Length 542;
 Best Local Similarity 31.9%; Pred. No. 3,7e-42;
 Matches 129; Conservative 91; Mismatches 158; Indels 27; Gaps 7;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPLHLDEEDYLGQARHMLSKVGMDFDIFL 121
 DB 104 KKKKQOQMLTQISGVYKLLHSSSLNNTSISRQVNTENEDHLAKLEDLNR--WGLNIFN 160
 QY 122 FDRLTNGNSLVTLTLCHEFTNGLIHHFKLDVYTLHFLVWQEDYHSQNPYHNAVHAADY 181
 DB 161 VAGYSNRPRLTGMATVAFQERDLTKFKISSDFTVYMKMTLEDYHSDVAVHNSLHAADY 220
 QY 182 TOAMHCYLKEPKLASFLPRDIMGLAAAHADVDHPGNOPFLIKTNHHLANLYONMSV 241
 DB 221 AOSTHYLLSPALDAVFTDLLEILAIIPAAIHVDHPGVSNQPLINTSELALMYNDESV 280
 QY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLSLATDINQNEFLTRKANH 299
 DB 281 LENHHLAVGFKLQEHCHDIFQNLTKKQOTLRKRVIDMYLATDMSKHSLLADLKTWVE 340
 QY 300 NKD-----LRLEDADRHFMQLQALKCADICNPCRITWMSKQSEVCEEFYRQGELEQ 353
 DB 341 TKKVTSSGVLLDNDYTRIQVLRNMYHCHADLSNPKLSLELRTQMDIMEEFPOQGDKE 400
 QY 354 KFELEISPLCNOQKDSIPSIQIGMSYIYEPLEFRAWHTGNSLTSENMLGHLAHNAQW 413
 DB 401 ERGMEISPMCDKHTASVKSQVGFIDYIVHPLMETWADLVQPD--ADLDLLEDRNMY 458
 QY 414 KSLLR-----QHRSGSSGSGPDHD---AGQTESEBOEGD 448
 DB 459 QSMIPQSPPLDERSRDCQGLMEKFOFELTLDEEDSEKPEKEG 503

RESULT 7
 ID 013945 PRELIMINARY; PRT; 606 AA.
 AC 013945;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE 3,5-CYCLIC AMP PHOSPHODIESTERASE (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93314968; PubMed=8392015;
 RA Oberholte R., Bhakta S., Alvarez R., Bach C., Mulkins M., Jarnagin K.,
 RA Shelton E.R.;
 RT "The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV)
 RT Gene 129:239-247(1993)."
 RL EMBL; L12686; AAA35643.1; -
 DR EMBL; L12686; AAA35643.1; -
 DR InterPro; IPR003607; HDC.

DR InterPro; IPR002073; PDEase.
 DR Pfam; PR00233; PDEase; 1
 DR PRINTS; PR00387; PDIESTERASEL.
 DR SMART; SM00471; HDC; 1
 DR PROSITE; PS00126; PDEASE_1; 1.
 KW CAMP.
 FT NON_TER 1 1
 SQ SEQUENCE 606 AA; 68663 MW; 256BD63B32C79398 CRC64;

Query Match 23.6%; Score 567.5; DB 4; Length 606;
 Best Local Similarity 31.3%; Pred. No. 1.4e-41;
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

QY 66 KKKVKRLS----FQRYFNASRLRGITPOAPLHLDEEDYLGQARHMLSKVGMDFDIFL 121
 DB 168 KKKKQOQMLTQISGVYKLLHSSSLNNTSISRQVNTENEDHLAKLEDLNR--WGLNIFN 224
 QY 122 FDRLTNGNSLVTLTLCHEFTNGLIHHFKLDVYTLHFLVWQEDYHSQNPYHNAVHAADY 181
 DB 225 VAGYSNRPRLTGMATVAFQERDLTKFKISSDFTVYMKMTLEDYHSDVAVHNSLHAADY 284
 QY 182 TOAMHCYLKEPKLASFLPRDIMGLAAAHADVDHPGNOPFLIKTNHHLANLYONMSV 241
 DB 285 AOSTHYLLSPALDAVFTDLLEILAIIPAAIHVDHPGVSNQPLINTSELALMYNDESV 344
 QY 242 LENHWRSTIGMLRESR--LLAHLPKEMTODIEQOLSLATDINQNEFLTRKANH 299
 DB 345 LENHHLAVGFKLQEHCHDIFQNLTKKQOTLRKRVIDMYLATDMSKHSLLADLKTWVE 404
 QY 300 NKD-----LRLEDADRHFMQLQALKCADICNPCRITWMSKQSEVCEEFYRQGELEQ 353
 DB 405 TKKVTSSGVLLDNDYTRIQVLRNMYHCHADLSNPKLSLELRYQMDIMEEFPOQGDKE 464
 QY 354 KFELEISPLCNOQKDSIPSIQIGMSYIYEPLEFRAWHTGNSLTSENMLGHLAHNAQW 413
 DB 465 ERGMEISPMCDKHTASVKSQVGFIDYIVHPLMETWADLVQPD--ADLDLLEDRNMY 522
 QY 414 KSLLR-----QHRSGSSGSGGP-----DHDHNG-----QGTSEBOEGD 448
 DB 523 QSMIPQ-----SPSPLEQNRDCQGLMEKFOFELTLDEEDSEKPEKEG 567

RESULT 8
 ID 09H3H2 PRELIMINARY; PRT; 825 AA.
 AC 09H3H2;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYCLIC AMP-SPECIFIC PHOSPHODIESTERASE HSPDE4A10.
 GN PDE4A.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRATN;
 RA Rena G., Begg F., Ross A., Mackenzie C., McPhee I., Campbell I.,
 RA Huston E., Sullivan M., Houslay M.D.;
 RT "Molecular cloning, genomic positioning, promoter identification and
 RT characterisation of the novel CAMP-specific phosphodiesterase,
 RT PDE4A10.";
 RL MOL. Pharmacol. 0:0-0(2001).
 DR EMBL; AF073745; AAD34217.2; -
 DR InterPro; IPR003607; HDC.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASEL.
 DR SMART; SM00471; HDC; 1
 DR PROSITE; PS00126; PDEASE_1; 1.
 SQ SEQUENCE 825 AA; 91322 MW; B50A342801E605FB CRC64;

SQ SEQUENCE 700 AA; 77600 MW; B39732360C2E18A5 CRC64;

Query Match 23.3%; Score 562; DB 4; Length 700;
Best Local Similarity 28.2%; Pred. No. 5,3e-41;
Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;

11 EILFENPDQNAKVCVMIGDIRLNGQTVRAERRGSTPFIDFRLN-----STYSG-- 61
192 KLALETDELDCIDOLETQOTRHVSQVEMASNKFK-----RLNRELTHLSETSRSGNQ 245
62 -----EIGTKK-----KVKRLSFORYFHASRLRGIIPOAPLHLD 99
246 VSEYISRTFLDQTEVELPKVTAEEAPQPMRSRISGLHGLCHSASLSATVPFRGVQTDQE 305
100 DYLGQARHMLSKVGMWDFIDFLFDRLTNGSLVTLCHLPHNGLIHFKLDMVTLHREL 159
306 EQLAKE---LEDTKMGDLDFKVAELSGNPLTAIFISIFOEERDLTKFOIPADTLATYL 362
160 VMQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHFG 219
363 LMLGHHANAVAHNSLHADVAOSTHVLATPALFAVFTDEILALFASAIHVDHFG 422
220 VNQFELIKTNHNLNLYONNSVLENHHRSTIGMLRESR--LLAHLPKEMTODIEQOLGS 277
423 VSNQFLINTSELNLMYNDASVLENHHLAVGFKLQAEKNDIFONLSAKORSLRMYVD 482
278 LILATDINRQNEFLTRKLAHLNND-----LRLEDAODRHEMLQIALKADICNCRITW 331
483 MYLATDMSKHMNLADIKTWEETKVTSLGVLLDNDSDRIQVQLMVLHACADLSNFTKPL 542
332 EMSKQSERVCEEFYRQGELEOKFELEISPLCNOQKDSIPSIQIGMSYIVELFKEMAH 391
543 PLYRWMTDRIAAEFPOODRERESGLDISPCCKHTASVKSQVGFIDYIAHLMETWAD 602
392 FTGNSTLSENNIIGHLAHNAKQMSLPRORHS--RGSSGSGPDH-----DHAGQTESE 443
603 LVHPD--AQDLDTLEDNREMYOSKIPRSPDLTPNPERDGPDRFOFELTLEAEDEDEE 660
444 EDEGD 448
1:1:1
DB 661 EEEGE 665

RESULT 11
076105 PRELIMINARY; PRT: 782 AA.
AC 076105;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
PDEAC-791 (FRAGMENT).
GN PDEAC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN NCB1_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Lemerding J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stijlgen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Gannes J., Avila J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Andreise T., Trankiel M., Amico-Keller G.,
RA Croftfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Saunders C., Ow D., Nolan M., Tring S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a ~600 kb region in 19p13.1 between JAK3 and
RT PDEAC".
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005759; AAC83050.1; --
DR InterPro; IPR003607; HDC.
DR InterPro; IPR002073; PDEase.

PFam: PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASL.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_1; 1.
FT NON_TER 1
SQ SEQUENCE 782 AA; 87342 MW; 4287F735F1C1D24 CRC64;

Query Match 23.3%; Score 562; DB 4; Length 782;
Best Local Similarity 28.2%; Pred. No. 6,2e-41;
Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;

11 EILFENPDQNAKVCVMIGDIRLNGQTVRAERRGSTPFIDFRLN-----STYSG-- 61
274 KLALETDELDCIDOLETQOTRHVSQVEMASNKFK-----RLNRELTHLSETSRSGNQ 327
62 -----EIGTKK-----KVKRLSFORYFHASRLRGIIPOAPLHLD 99
328 VSEYISRTFLDQTEVELPKVTAEEAPQPMRSRISGLHGLCHSASLSATVPFRGVQTDQE 387
100 DYLGQARHMLSKVGMWDFIDFLFDRLTNGSLVTLCHLPHNGLIHFKLDMVTLHREL 159
388 EQLAKE---LEDTKMGDLDFKVAELSGNPLTAIFISIFOEERDLTKFOIPADTLATYL 444
160 VMQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLASFLTPDLMGLLAAAHVDHFG 219
445 LMLGHHANAVAHNSLHADVAOSTHVLATPALFAVFTDEILALFASAIHVDHFG 504
220 VNQFELIKTNHNLNLYONNSVLENHHRSTIGMLRESR--LLAHLPKEMTODIEQOLGS 277
505 VSNQFLINTSELNLMYNDASVLENHHLAVGFKLQAEKNDIFONLSAKORSLRMYVD 564
278 LILATDINRQNEFLTRKLAHLNND-----LRLEDAODRHEMLQIALKADICNCRITW 331
565 MYLATDMSKHMNLADIKTWEETKVTSLGVLLDNDSDRIQVQLMVLHACADLSNFTKPL 624
332 EMSKQSERVCEEFYRQGELEOKFELEISPLCNOQKDSIPSIQIGMSYIVELFKEMAH 391
625 PLYRWMTDRIAAEFPOODRERESGLDISPCCKHTASVKSQVGFIDYIAHLMETWAD 684
392 FTGNSTLSENNIIGHLAHNAKQMSLPRORHS--RGSSGSGPDH-----DHAGQTESE 443
685 LVHPD--AQDLDTLEDNREMYOSKIPRSPDLTPNPERDGPDRFOFELTLEAEDEDEE 742
444 EDEGD 448
1:1:1
DB 743 EEEGE 747

RESULT 12
043849 PRELIMINARY; PRT: 791 AA.
AC 043849;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
PDEAC-791 (PDEAC-426) (FRAGMENT).
GN PDEAC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN NCB1_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Tissue-Testis;
RA MEDLINE-95145731; PubMed-7843419;
RA Engels P., Sullivan M., Muller T., Lubbert H.;
RT "Molecular cloning and functional expression in yeast of a human CAMP-
RT specific phosphodiesterase subtype (PDE IV-C).";
RL Febs Lett. 358:305-310(1995).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE-TESTIS, AND LUNG;

RX MEDLINE=98007880; PubMed=9349724;
 RA Ojornito R., Ratzliff J., Baecker P.A., Daniels D.V., Zuppan P.,
 RA Jernagin K., Shelton E.R.;
 RT "Multiple splice variants of phosphodiesterase PDE4C cloned from human
 RT lung and testis";
 RL Biochim. Biophys. Acta 1353:287-297(1997).
 DR EMBL; U66346; AAB96875.1; -;
 DR EMBL; U66347; AAB96876.1; -;
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 FT NON_TER 1
 FT SEQUENCE 791 AA; 88142 MW; 616F606E39719B8 CRC64;

Query Match 23.3%; Score 562; DB 4; Length 791;
 Best Local Similarity 28.2%; Pred. No. 6.3e-41;
 Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;

QY 11 EILENPQNAKCYCMGDIKRCQGYRAERGSYPIIDRLN-----STTYSG-- 61
 DB 283 KIALETIDELDMCIDOLETQTRHSGEMASNKPK-----RIINRELTHLSETSRSQ 336
 QY 62 -----EIGTKK-----KYKRLSFQRYFHASRLGIIPOAPLHLDE 99
 DB 337 VSEIISTKFLDOOTEVELEPKYTAEEAPQPMKRIISGLHGLCHSASLTATVFRGVQDOE 396
 QY 100 DYLGQARHMLSKVGMDFDIFLFDRLTNGNSLVTLCHLFNTGILHHFKLDVTLHREFL 159
 DB 397 EQLAKE---LEDTKMGGLDVKVAELSGNQPLTAIFSIIFQERDLTKFQIPADTLATYL 453
 QY 160 VMQVEDHSQRYNNAVAADVQAMHCYKLEPKLASFLPLDMLGILAAAHADVHPG 219
 DB 454 LMLGHHYANVAHNSHAAVQSTHVLATPALAEVDTLEILAAEFASAIHDVHPG 513
 QY 220 VNQFLLKTNHNLNQNMSVLENHHRSTIGMLRESR--LLAHLPRKEMQDIEQOLGS 277
 DB 514 VSNQFLINTNSLALMNDASVLENHHLAVGFKLQAEKNCIFQNLASKOKSLRMYID 573
 QY 278 LIALTDINRQNEFLTRKLAHLNKKD-----LRLEDADRHFMLQALKCADICNPRIM 331
 DB 574 MYLATDMSKHMNLLADIKTWEYTKKVTSLGVLIDNYSRQIYVNLVHCADLSNPKPL 633
 QY 332 EMSQWSEVCEEFYRQGELEOKFELEISPLCNOOKDSIPSIQIGFMSYIEPLFREMAH 391
 DB 634 PLYRQMTDRIMAEFFQOGDREREGSLDISPMCDKHTASVEKSYQGFIDYIYHPIMETWAD 693
 QY 392 FTGNTSTSENNLGLAHNKAQWKSLLPRQHS--RGSSSGSGPDH-----DHAGQGTSE 443
 DB 694 LVHPD--AQDILDTLEDNRKWTQSKIRPSDGLTNPERRGDPROFELTLEAEEDDEE 751
 QY 444 EOEED 448
 DB 752 EEED 756
 RESULT 13
 Q9EOR7 PRELIMINARY; PRT; 771 AA.
 AC Q9EOR7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CYCLIC AMP PHOSPHODIESTERASE PDE4A10 (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Rana G., Begg F., Ross A., Mackenzie C., McPhee I., Campbell L.,
 RA Huston E., Sullivan M., Houslay M.D.;
 RT "Molecular cloning, genomic positioning, promoter identification and
 RT characterisation of the novel cAMP-specific phosphodiesterase,
 RT PDE4A10";
 RL Mol. Pharmacol. 0:0-0(2001).
 DR EMBL; AF110461; AAF14352.2; -;
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 FT NON_TER 1
 FT SEQUENCE 771 AA; 85459 MW; D20712E515CDAFOB CRC64;

Query Match 23.2%; Score 559.5; DB 11; Length 771;
 Best Local Similarity 31.1%; Pred. No. 1e-40;
 Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;

QY 43 RGSYPIFDRLNNTTSGELGKTKKRYRLSFQRYFHASRLGIIPOAPLHLDEYL 102
 DB 241 RQSPMSQITGLKRLVHSGSLNTN-----VRFVGTQDOEDLL 278
 QY 103 GQARHMLSKVGMDFDIFLFDRLTNGNSLVTLCHLFNTGILHHFKLDVTLHREFLMV 162
 DB 279 AQELEENKSK---KGLNIFVSEYAGNSLSCIMWTIIFQERDLKFFHLPVTMMYMLTL 335
 QY 163 QEDYHSQRYNNAVAADVQAMHCYKLEPKLASFLPLDMLGILAAAHADVHPGVNQ 222
 DB 336 EDHYADVAHYNNSHAAVQSTHVLATPALDAVETDLEILAAEFASAIHDVHPGVS 395
 QY 223 PFLKTNHNLNQNMSVLENHHRSTIGMLRESR--LLAHLPRKEMQDIEQOLGSLIL 280
 DB 396 QFLINTNSLALMNDASVLENHHLAVGFKLQAEKNCIFQNLASKOKSLRMYIDMV 455
 QY 281 ATDINRQNEFLTRKLAHLNKKD-----LRLEDADRHFMLQALKCADICNPRIMWS 334
 DB 456 ATDMSKHMNLLADIKTWEYTKKVTSSGVLIDNYSRQIYVNLVHCADLSNPKPLLEY 515
 QY 335 KQWSEVCEEFYRQGELEOKFELEISPLCNOOKDSIPSIQIGFMSYIEPLFREMAHFTG 394
 DB 516 RQMTDRIMAEFFQOGDREREGSLDISPMCDKHTASVEKSYQGFIDYIYHPIMETWADLVH 575
 QY 395 NSTSENNLGLAHNKAQWKSLLPRQHS--RGSSSGSGPDH-----DHAGQGTSE 441
 DB 576 PD--AQDILDTLEDNR--DW-----YHSAIRQSPSPLEERGGIGHPSLPDKFOFELTL 626
 QY 442 SEEOEDS 449
 DB 627 EEED 634
 RESULT 14
 Q9UPJ5 PRELIMINARY; PRT; 426 AA.
 AC Q9UPJ5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PDE4C-426.
 GN PDE4C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,

RA Danganan L., Poundstone P., Christensen M., Georgescu A., Ayala J.,
 RA Liu S., Atlix C., Andreise T., Frankheim M., Amico-Kelly C.,
 RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas R., Quan G.,
 RA Krommiller B., Arellano A., Saunders., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Gattino A.V.,
 RT Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
 RT PDE4C.
 RL EMBL: AF005759; AAC83049.1; -
 DR EMBL: AF005759; AAC83049.1; -
 DR InterPro: IPR003607; HDc.
 DR Pfam: PF00233; PDEase.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00471; HDc; 1.
 DR PROSITE: PS00126; PDEASE_1; 1.
 SO SEQUENCE 426 AA; 47870 MW; D29CEA570AC86A9A CIRC64;

Query Match 23.2%; Score 558.5; DB 4; Length 426;
 Best Local Similarity 30.8%; Pred. No. 5,6e-41;
 Matches 122; Conservative 82; Mismatches 171; Indels 21; Gaps 6;
 QY 69 VKRLSFQRYFHASRLNGITIPQAPRHLDEEDYLGQARHMLSKVGMDFDIFEDRLTNG 128
 DB 1 MSRLSGHGLCHSASLSATYPRFGVOTDDEQLAKE--LEDTKNGLDVFKVAELSGN 57
 QY 129 NSLVTLLCHLNTFHTGLIHFKLDVNTLRPLVWVQEDYHSQNPYHNAVHADYTOAMHCY 188
 DB 58 RPLTAIIFSIQERDLTKTQIPADTLATYLLMEGHYHANVAVHNSLHADVAOSTHYL 117
 QY 189 LKEPKLASFLPLDIMGLLAAAHVDVHPCVNOPEFLIKTNHLLANLYONKSYLENHMR 248
 DB 118 LATPALEAVFTLELALFASALHDVDPGVSNQFLINTSELAIMYNDASYLENHHLA 177
 QY 249 STIGMLRESR--LALHPKEMTODIEOGLSLIATDINRONEFLTRKALHAKND--- 302
 DB 178 VGEKLLQANFCDFONLSAKORLSRRMYIDVLTATDMSKHNMLADLKTWEYERKVTSL 237
 QY 303 --LLEEDADRRHFMQIALKCADICNPCRIMESKOWSERVCEFFYRGOLEOKFELEIS 360
 DB 238 GVLIDNYSDRIOVONLVHCADLSNPKPLRYQWTDRIWAEPFOGDREESGLDIS 297
 QY 361 PFCNOQKDSIPSIQIGFMSYIPELFRWAHFTGNSLENMGLHIANKQAMSLPRQ 420
 DB 298 PMCDKHTASVEKSGVGFIDYIAHPLMETWADLVHPD--AQDLLDTLEDNREMYOSKITPRS 355
 QY 421 HRS-RGSSGSGPDH-----DHAGGTSESEQED 448
 DB 356 PSDLTNPERDGPDRFOFELTLEAEDEDEDEEEGE 391

RESULT 15
 O9UN44 PRELIMINARY; PRT; 606 AA.
 ID O9UN44
 AC O9UN44
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CAMP SPECIFIC PHOSPHODIESTERASE PDE4C2 VARIANT.
 GN PDE4C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20039485; PubMed-10574328;
 RA Sullivan M., Olsen A.S., Houslay M.D.,
 RT "Genomic organization of the human cyclic AMP-specific
 RT phosphodiesterase PDE4C gene and its chromosomal localisation to
 RT 19p13.1, between RAB3A and JUND."
 RT Cell. Signal. 11:735-742(1999).
 RL EMBL: AF157816; AAD47055.1; -

DR EMBL: AF157814; AAD47055.1; JOINED.
 DR EMBL: AF157815; AAD47055.1; JOINED.
 DR InterPro: IPR003607; HDc.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00471; HDc; 1.
 DR PROSITE: PS00126; PDEASE_1; 1.
 SO SEQUENCE 606 AA; 67824 MW; 0C42PC922E3B798 CIRC64;

Query Match 23.2%; Score 558.5; DB 4; Length 606;
 Best Local Similarity 30.8%; Pred. No. 3e-41;
 Matches 122; Conservative 82; Mismatches 171; Indels 21; Gaps 6;
 QY 69 VKRLSFQRYFHASRLNGITIPQAPRHLDEEDYLGQARHMLSKVGMDFDIFEDRLTNG 128
 DB 181 MSRLSGHGLCHSASLSATYPRFGVOTDDEQLAKE--LEDTKNGLDVFKVAELSGN 237
 QY 129 NSLVTLLCHLNTFHTGLIHFKLDVNTLRPLVWVQEDYHSQNPYHNAVHADYTOAMHCY 188
 DB 238 RPLTAIIFSIQERDLTKTQIPADTLATYLLMEGHYHANVAVHNSLHADVAOSTHYL 297
 QY 189 LKEPKLASFLPLDIMGLLAAAHVDVHPCVNOPEFLIKTNHLLANLYONKSYLENHMR 248
 DB 298 LATPALEAVFTLELALFASALHDVDPGVSNQFLINTSELAIMYNDASYLENHHLA 357
 QY 249 STIGMLRESR--LALHPKEMTODIEOGLSLIATDINRONEFLTRKALHAKND--- 302
 DB 358 VGEKLLQANFCDFONLSAKORLSRRMYIDVLTATDMSKHNMLADLKTWEYERKVTSL 417
 QY 303 --LLEEDADRRHFMQIALKCADICNPCRIMESKOWSERVCEFFYRGOLEOKFELEIS 360
 DB 418 GVLIDNYSDRIOVONLVHCADLSNPKPLRYQWTDRIWAEPFOGDREESGLDIS 477
 QY 361 PFCNOQKDSIPSIQIGFMSYIPELFRWAHFTGNSLENMGLHIANKQAMSLPRQ 420
 DB 478 PMCDKHTASVEKSGVGFIDYIAHPLMETWADLVHPD--AQDLLDTLEDNREMYOSKITPRS 535
 QY 421 HRS-RGSSGSGPDH-----DHAGGTSESEQED 448
 DB 536 PSDLTNPERDGPDRFOFELTLEAEDEDEDEEEGE 571

Search completed: September 13, 2002, 12:08:55
 Job time: 241 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 12:02:04 : Search time 20.91 Seconds
(without alignments)
2067.920 Million cell updates/sec

Title: US-09-471-459a-5

Perfect score: 2408

Sequence: 1 MSCLMWERCCELLFENPDQN.....PDHDAQGCTESESQESDSP 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	2408	100.0	450	2	JC7266 3',5'-cyclic-nucle
2	1419.5	58.9	498	2	A47286 3',5'-cyclic-AMP p
3	604.5	25.1	673	2	161358 3',5'-cyclic-nucle
4	603.5	25.1	584	2	B51209 3',5'-cyclic-nucle
5	580.5	24.1	672	2	161259 3',5'-cyclic-nucle
6	580.5	24.1	562	2	159143 CAMP phosphodiesterase
7	580.5	24.1	564	2	A40949 cyclic-AMP phospho
8	567.5	23.6	564	2	JC1519 3',5'-cyclic-nucle
9	567.5	23.6	736	2	161354 phosphodiesterase
10	565	23.5	886	2	A54442 3',5'-cyclic-nucle
11	559.5	23.2	610	2	167946 3',5'-cyclic-nucle
12	559.5	23.2	844	2	153865 phosphodiesterase
13	553	23.0	712	2	S71626 3',5'-cyclic-nucle
14	529.5	22.0	536	2	167945 3',5'-cyclic-nucle
15	517	21.5	549	2	T16769 hypothetical prote
16	493	20.5	777	2	S65543 3',5'-cyclic-nucle
17	477.5	19.8	323	2	S55348 3',5'-cyclic-nucle
18	468	19.4	267	2	B33904 CAMP phosphodiesterase
19	468	19.4	535	1	A46378 3',5'-cyclic-nucle
20	467	19.4	534	1	A44162 3',5'-cyclic-nucle
21	466	19.4	519	2	T14783 hypothetical prote
22	466	19.4	535	1	A44161 3',5'-cyclic-nucle
23	461	19.1	664	2	T24459 hypothetical prote
24	454.5	18.9	530	1	A45334 3',5'-cyclic-nucle
25	452.5	18.8	768	2	T10796 3',5'-cyclic-nucle
26	449	18.6	536	1	JC6129 3',5'-cyclic-nucle
27	445.5	18.5	713	2	JM0088 3',5'-cyclic-nucle
28	441	18.0	659	2	JE0293 3',5'-cyclic-nucle
29	409	17.0	491	2	A40283 3',5'-cyclic-nucle

30	381	15.8	875	1	JM0106 3',5'-cyclic-GMP p
31	377	15.7	875	1	A48719 3',5'-cyclic-GMP p
32	370	15.4	1054	2	T13901 cyclic nucleotide
33	368.5	15.3	1112	2	S70522 cyclic nucleotide
34	357.5	14.8	1108	2	A48508 cyclic-nucleotide
35	346	14.4	1141	2	A44093 cGMP-inhibited cam
36	302.5	12.6	858	2	JC4520 3',5'-cyclic-GMP p
37	300	12.5	855	2	A34810 3',5'-cyclic-GMP p
38	299	12.4	928	1	JC2486 3',5'-cyclic-nucle
39	296	12.3	921	1	A40981 3',5'-cyclic-nucle
40	283	11.8	853	2	A36617 3',5'-cyclic-GMP p
41	279	11.6	856	1	A47451 3',5'-cyclic-GMP p
42	278	11.5	856	2	S30762 3',5'-cyclic-GMP p
43	277.5	11.5	854	2	A42828 3',5'-cyclic-GMP p
44	269.5	11.2	862	2	I50186 3',5'-cyclic-GMP p
45	268	11.1	859	2	B34611 3',5'-cyclic-GMP p

ALIGNMENTS

RESULT 1

JC7266

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human

N:Alternate names: CAMP-specific phosphodiesterase 7B

C:Species: Homo sapiens (man)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000

C:Accession: JC7266

R:Sasaki, T.; Kotera, J.; Yusa, K.; Omori, K.

Biochem. Biophys. Res. Commun. 271, 575-583, 2000

A>Title: Identification of human PDE7B, a CAMP-specific phosphodiesterase.

A:Reference number: JC7266

A:Accession: JC7266

A:Molecule type: mRNA

A:Residues: 1-450 <SAS>

A:Cross-references: DDBJ:AB038040

A:Experimental source: caudate nucleus

C:Genetics:

A:Gene: pde7B

A:Map position: 6q23-24

C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'

C:Keywords: phospholipid diester hydrolase

Query Match	100.0%	Score 2408	DB 2	Length 450
Best Local Similarity	100.0%	Pred. No. 1.2e-183		
Matches 450	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSCLMWERCCELLFENPDQNAKVCMLGDIRLGGTGVBAERGSYPFLDFRLNSTYS 60		
DB	1	MSCLMWERCCELLFENPDQNAKVCMLGDIRLGGTGVBAERGSYPFLDFRLNSTYS 60		
QY	61	GEIGTKKKVKRLISFQRYRHASRLRGITIPQAPLHLLDEYLGQAHHMISKGMDFDTF 120		
DB	61	GEIGTKKKVKRLISFQRYRHASRLRGITIPQAPLHLLDEYLGQAHHMISKGMDFDTF 120		
QY	121	LPDRRLNGNSIVTLGHLNFTGHLHHFKLIDWTLRLFLMVOEDYHSONPYNAVAHAD 180		
DB	121	LPDRRLNGNSIVTLGHLNFTGHLHHFKLIDWTLRLFLMVOEDYHSONPYNAVAHAD 180		
QY	181	VTOAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240		
DB	181	VTOAMHCYKEPKLASFLPLDIMGILAAAHVDHPCVNOPEFLTKTNHNLANTYONNS 240		
QY	241	VLENHWRSTIGMLRSRLLAHLPKMTODIEQOLGSLIADDDINQNEFLRLKAHLN 300		
DB	241	VLENHWRSTIGMLRSRLLAHLPKMTODIEQOLGSLIADDDINQNEFLRLKAHLN 300		
QY	301	KDLRLDADDRHMLDIALKADICNPCRITWESKOWSERVEEYFROGELROKPLETS 360		
DB	301	KDLRLDADDRHMLDIALKADICNPCRITWESKOWSERVEEYFROGELROKPLETS 360		
QY	361	PLCNOQKDSIPSIQIGFMSYIVEPLFERMAHFTGNSITSENMIGLHANNAKQKSLPQ 420		

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|||||
Db 361 PLCNQOKDSIPSTIGFMSYVEPLFREMAHFTGNSTLSNMGLAHNKAQKSLRPQ 420
QY 421 HRSRSGSGSPDHDAAGGTSEDEGDSR 450
Db 421 HRSRSGSGSPDHDAAGGTSEDEGDSR 450

RESULT 2
A47286
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000
C:Accession: A47286
R:Michaelli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers
J. Biol. Chem. 268, 12925-12932, 1993
A:Title: Isolation and characterization of a previously undetected human cAMP phosphodi
A:Reference number: A47286; MUID:93286141
A:Accession: A47286
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-498 <MTC>
A:Cross-references: GB:U12052; NID:q179892; PID:q179893
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C:Keywords: phosphoric diester hydrolase
F:227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

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Query Match 58.9%; Score 1419.5; DB 2; Length 498;
Best Local Similarity 61.7%; Pred. No. 5.4e-105;
Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERCEILFENPDQAKVCMLGDIRRGCTGVFAERGSYFDFPLNSTTSGEIDTK 66
Db 62 QRRGALSYDSDQATATYRMIGDVRRVRAGFESESRGSHPTIDPRIFHSEIEVSVA 121
QY 67 KKVRLSPQRYFASRLRGITRQAPRLHLLDEDTYGOARHMLSKVGMDDPFIPLDT 126
Db 122 RNIRRLSPQRYLRSSRFPGTAVSNLSLDDDTYNGQAKCLEYKGNMDFIPLDT 181
QY 127 NGNSLVTLCHLFTHTLHFKLDVTLHRLVYMGQYHSONYHNAVAADVTQAM 186
Db 182 NGNSLVTLHFLSLHGLIEYFDHMKARFLVMDQEDYHSONYHNAVAADVTQAM 241
QY 187 CYKKEPKLAFPLRDLIMGLAAAHADVDPGVNQPFLITKTNHLLANLYONMSYLENN 246
Db 242 CYLEKPLANSVTPWDLISLAATHDLDHGVNQPFLIKTNHLLATLYKNTSLENH 301
QY 247 WRSTIGLRSLIAHLPEKMTODIEQOLGSLIATDINRONFELTRKALHNNKDLRL 306
Db 302 WRSVAVGLRRESGLFSLPLESRQOMETQIGALITDISRQNEYLSLFRSHLDGDCLE 361
QY 307 DAODRHFMLQALKCADICNFCRIMESKMSERVICEEYFGELQEFELISPLCNOQ 366
Db 362 DTRHRLVYLOMALCADICNFCRTWELSKMSEKYEFEFPGQDIKKYHGVAPLDRH 421
QY 367 KDSIPSTIGFMSYVEPLFREMAHFTGNSTLSNMGLAHNKAQKSLRPDRHRSRG 426
Db 422 TESIANIQIGFMTYVEPLFTEWARS-NTRLSQTMILGHVGLNKAQKGLDREGSSSDT 480
QY 427 SGS 429
Db 481 DAA 483

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RESULT 3
I61358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific - human
N:Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C:Accession: I61358; I38416
R:Boiger, G.; Michaelli, T.; Martine, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,

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Mol. Cell. Biol. 13, 6558-6571, 1993
A:Title: A family of human phosphodiesterases homologous to the dunce learning and me
A:Reference number: A54442; MUID:94019330
A:Accession: I61358
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-673 <RES>
A:Cross-references: GB:U20970; NID:9347129; PIDN:AAA03592.1; PID:9347130
R:Becker, P.A.; Obermole, R.; Bach, C.; Yee, C.; Shelton, E.R.
Gene 138, 253-256, 1994
A:Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodi
A:Reference number: I38416; MUID:94171048
A:Accession: I38416
A:Molecule type: mRNA
A:Residues: 70-507; P, 509-673 <RE2>
A:Cross-references: EMBL:U02882; NID:9433346; PIDN:AAIC13745.1; PID:9433347
A:Gene: GDB:PD63
A:Cross-references: GDB:132541; OMIM:600129
A:Map position: 5q12-5q12
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
C:Keywords: cAMP binding; phosphoric diester hydrolase
F:325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

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Query Match 25.1%; Score 604.5; DB 2; Length 673;
Best Local Similarity 33.3%; Pred. No. 5.1e-40;
Matches 135; Conservative 86; Mismatches 131; Indels 33; Gaps 9;

QY 66 KKVRLKLS----FQRYFASRLRGITRQAPRLHLLDEDTYGOARHMLSKVGMDDPFIPL 121
Db 218 KKKKRPMSQIGCVKRLMSSLSIPRGVTEDEYLAKE--LELVNKGGLHYR 274
QY 122 FDLRLNGSLVTLCH-LENTGLINHPKLDVTLHRLVYMGQYHSONYHNAVAADVTQAM 180
Db 275 IREL-SGNRPVLVIMHTTFOERDLTKFERIVDTLYLMTLEDYHADVAHNNIHAAD 333
QY 181 VTQAMHCYLEPKLASFLRDLIMGLAAAHADVDPGVNQPFLITKTNHLLANLYONMSYLENN 240
Db 334 VVOSTHVLTLSTPALAVFTDLEILAIFASAIIHVDHGVSNQELLNTNSELALMTNDS 393
QY 241 VLENHNRSTIMLEESR--LLAHLPKEMTODIEQOLGSLIATDINRONFELTRKALH 298
Db 394 VLENHILAVGFKLQEEKNDIFQNLTKRQSRKRVIVLAVTDMSKHNNLLADLKTIV 453
QY 299 HKND-----RLFEADQDRHMLQALKCADICNFCRIMESKMSERVICEEYFGEL 352
Db 454 ETKVYSSGVLLDNYSPRIQVLONNYHCADLSNTPKFDLYKQWTDRIEERFGQDRE 513
QY 353 OKFELISPLCNOQDSIPSTIGFMSYVEPLFREMAHFTGNSTLSNMGLAHNKAQ 412
Db 514 RERGMEISPMCKDKNHNASVEKSOVFIDYIVHFLVETVADLVHPD--AODLTLLEDNRW 571
QY 413 KWSLLPDRHRSRGSGSPDHDAAGGTSE-----EDEGDS 449
Db 572 YOSTLIPQ-----SPSPADDPDEGRGQTEKFOFELTLEDEGS 610

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RESULT 4
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice for
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B53109; A34414; C33904; I67944
R:Monaco, L.; Vicini, E.; Confi, M.
J. Biol. Chem. 269, 347-357, 1994
A:Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP
A:Reference number: A53109; MUID:94103234
A:Accession: B53109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <MON>
A:Cross-references: GB:U01280

```


R.Suvinen, J.V., Joseph, D.R.; Contli, M.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
 A>Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormones
 A:Reference number: A34414; MUID:90045763
 A:Accession: A34414
 A:Molecule type: mRNA
 A:Residues: 1-584 <SMN>
 A:Cross-references: GB:U09455; GB:M25349; NID:g517501; PIDN:AAA20401.1; PID:g517502; GB:U09455
 R.Suvinen, J.V.; Joseph, D.R.; Contli, M.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
 A>Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP PDE
 A:Reference number: A33904; MUID:89315790
 A:Accession: C33904
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 214-480 <SMW2>
 A:Cross-references: GB:M25349
 R.Bolger, G.B.; Rodgers, L.K.; Riggs, M.
 Gene 149, 237-244, 1994
 A>Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
 A:Reference number: I53865; MUID:95047482
 A:Accession: I67944
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 'EPGGS', 34-421, 'E', 423-584 <RES>
 A:Cross-references: GB:I27060; NID:g436009; PID:g436010
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1b, calmodulin-dependent; 3',5'-cyclic-nucleotide phosphodiesterase 1b, calmodulin-dependent; cAMP binding; phosphoric diester hydrolase
 F:237-465/domian: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match	25.1%;	Score 603.5;	DB 2;	Length 584;
Best Local Similarity	33.3%;	Pred. No. 5e-40;		
Matches 135;	Conservative 85;	Mismatches 152;	Indels 33;	Gaps 9;

Qy	66	KKKVKRLLS----	FORFHXARLLRGITIPARLHLEDELYGOKRNYLSVGMWDFIFL	121
Db	130	KEKKRRPMSQJSGYKAKMLHSSSLNSCIPRGVATDEEDYLAKE---	LEDMKKGLHYFR	166
Qy	122	FDRLTNGSLVTLTLLCH--LENTGHILNHEKLDMTLHARFLVWOEDYNSQPNYHNAVHAD	180	
Db	187	IAEL--SGNRPLVLTMHTLIFQGRDCLKTFKFIQVDTLITLMTLEDPHYHADAVALYNNHTIAAD	245	
Qy	181	VTQAMCSTLKPERKLAASEFLPDIYDLIGLAAARADVHRCVGNQRPFLKTNHNLANTLONMS	240	
Db	246	VWOSTHVLSTPRALEAVFTDLEITIAAFASAIHBDVHDPAGVSNQFLINTNSELALMYNDSS	305	
Qy	241	VLENNHNMSTIGMLRESR--LLALPRKEMODIEQGLSLATDTRKQNEFLTRLKAKHL	298	
Db	306	VLENNHNLAVGFKLLDOENCDFEONLTKKQROSLKMAIDIVLATDMSEKHNMLADLAKTMY	365	
Qy	299	HNKD-----LRLDADDRHFMLOITALKCADICNPRKIMESKOWSERVEEFGROGELE	352	
Db	366	ETKAVTSSGVLILLDNYISRILOYLONMYHCADLSNPTRYPLQYKRWMDRIEMEEFROGDRE	425	
Qy	353	QKFELEISPLCNOQKDSIPSLQIGFMSYIYERPLEREWAHFTGNSTSENNLGHILAHNKAQ	412	
Db	426	RERGRMEISPMCDKHNASYERQSQVGFIDYIYHARLEWTADVLVHPD--AQDILDTLEDNREW	483	
Qy	413	WKSLLPRQHRKSSGSGSPRHDAHAGQTESE-----EQEGDS	449	
Db	484	YOSTIPQ-----SPSPAPDQDEGRGQGEKQFQELTLEDEDS	522	

RESULT 5
161259 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form F
N:Alternate names: cyclic-AMP phosphodiesterase
C:Contents: 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, s
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence-revision 02-Jul-1996 #text-change 17-Nov-2000
C:Accession: 161259, A53678, I67943
C:Sette, C.; Vicini, E.; Conti, M.

J. Biol. Chem 269, 18271-18274, 1994
A:Title: The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins differ
A:Reference number: A53678; MUID:94308045
A:Accession: 161259
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-672 <RES>
A:Cross-references: EMBL:U09457; NID:g517418; PID:g517419
A:Accession: A53678
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 167-672 <RE2>
A:Cross-references: EMBL:U09456; NID:g517416; PIDN:AAA20393.1; PID:g517417
R:Bolger, G.B., Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian g
A:Reference number: I53865; MUID:95047482
A:Accession: 167943
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'N', 96-625, 'Y', 627-672 <RE3>
A:Cross-references: GB:I27059; NID:g436007; PIDN:AAA56857.1; PID:g436008
C:Genetics:
A:Gene: PDE3/IVd gene
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3
C:Keywords: cAMP binding; phosphoric diester hydrolase
I:323-553/Domains: 3,5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match	25.1%;	Score 603.5;	DB 2;	Length 672;
Best Local Similarity	33.3%;	Pred. No. 6.1e-40;		
Matches 135;	Conservative 85;	Mismatches 152;	Indels 33;	Gaps 9;

QY	66	KKKYKRLLS-----FOQFHHASRLRGITIPAPRLHLLDEDVIGARHNLSTYGVMMDEIFL	120
Db	218	KEKKRRPMSQJSGYKMLHSSSLTNSCIPRGYKTBEDVDLAKF---LEBNKKMGHLHYFR	274
QY	122	FDRLTNGSLVLTLLCH-LFNTHGILHHFKLDMVTLHARFLVWQVDYHSONPYNHVAHAD	180
Db	275	IAEL-SGNRPFLTYIMHTTFQBRDLTKTFKFIIPVDTLTYLMTLEDDHYHADVAHNNHIAAD	333
QY	181	VTQAMHCYKLPKPLASTLPRLDMLGGLAAARDVHNRGVNOFPLKLTNNHNLANYONMS	240
Db	334	VVOSTHYLLSTPALEAAFTDLEIILAAIFASAIHVDHVRGVSNOFLINTNSELMLAMDSS	393
QY	241	VLENNHMRSTIGMLRESR--LHAFKPMETODIQOQSGSLIATDRIQONREPLTRYKAHL	298
Db	394	VLENNHNLAVGKRLILOEENCDFIOWULTKKOROSLKKAAIDIVLTATMSKKNHNLADLKTMY	453
QY	299	HNKD-----LREDAODRHEMLDIALKCADICNCPRIWMSKOWSERVCEFEYRQGELE	352
Db	454	ETKRVTSGVLLDNTYSDRIQVLOLNMVHCADLSNPTKRPDLQYRWMDRIIMEFFRQGDRE	513
QY	353	QKFELEISPLCNOOKDSIPSTIQIGFMSYIYEPLEFREMAHFTGNSJTSENMLGHLANKAO	412
Db	514	RERMETISPMQDKINAAVEXKSGVGFIDYIYHNPETWADLVHPD--AODILDTLEDNREW	571
QY	413	IKXSLTPROHRSRGSSGSGPRDHAGQGTSE-----EQRDS 449	
Db	572	YQSTLPO-----SPAPRDQEDRGQGTQKTFQFLELDEDS 610	

RESULT 6
CAMP phosphodiesterase - rat (fragment)
I59143
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
C:Accession: I59143
R:Colicelli, J.; Birnmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A:Title: Isolation and characterization of a mammalian gene encoding a high-affinity
A:Reference number: I59143; MUID:89264471
A:Accession: I59143

A:Cross-references: GB:M97515; NID:g292387; PIDN:AAA36426.1; PID:g292388
 A:Experimental source: frontal cortex
 A:Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBI:P.127930)
 R:Boiger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993
 A:Title: A family of human phosphodiesterases homologous to the dunce learning and memory
 A:Reference number: A54442; MUID:94019330
 A:Accession: 161359
 A:Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-564 <RES>
 A:Cross-references: GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:g347132
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
 C:Keywords: phosphoric diester hydrolase
 F:233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 564;
 Best Local Similarity 31.3%; Pred. No. 3.5e-37;
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;
 QY 66 KKKVKKRLS-----FQRYFHASRLRLGIIIPQAPRLHLDLDEYLGQARHMLSKVGMDFDEL 121
 126 KKKQOQMTQISGVKKLMHSSLNNTSISRGVNTENDHAKLEEDLNK--WGLNIFN 182
 QY 122 FDRLTNGNSLVTLCHLFNTHGLIHFKLDVTLHRLVWQEDYHSQNPYHNAVHADV 181
 183 VAGSHNRPLICIMYALFOERDILKTRISSDTFTYMTLEDHYHSAVAHNSLHADV 242
 QY 182 TOAHNCYKLEPKLASFLPLDLMGLAAAHADVHGVPNPFLIKTNHNLANTYONKSV 241
 243 AOSTHVLSTPALDAVFTDEILIAIFAAIHVDHGVSNQFLINTSELTALMYNDESV 302
 QY 242 LENHNRSTIGMLRESR--LLAHLPKEMTODIEOGLSLATDINRQNEFLTRKALH 299
 303 LENHNLAVGFKLQDEHODIFMNLTKKQROQLRKMYIDVMTATMSKMSLLADKTWE 362
 QY 300 NKD-----LRLDAORHFMLOIALKADICNCRITWEMSKSERVECFYRQGELEQ 353
 363 TKKVTSSGVLLDDVYTRIGVLRMMVHCADLSNPTKSLEYRQWTDRIEMEFPOQDGER 422
 QY 354 KFELEISPLCNOQKDSIPISQIGFMSYIVPELPFEMAHFTGNSTLSENMLGHLANKAOW 413
 423 ERGMEISPMCDKHTASVEKSGVGFIDYIVHPLMETWADLVOPD--AQDILDTLEDNRMY 480
 QY 414 KSLPLRQHRSGSGSGP-----DHDHAG-----QGTSEEQEED 448
 481 QSMTPQ-----SPSPPLDEQNRDCQGLMEKFOFELTLDEDESGPERKEGE 525

RESULT 9
 161354
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence.revision 06-Sep-1996 #text_change 17-Nov-2000
 C:Accession: 161354
 R:Boiger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993
 A:Title: A family of human phosphodiesterases homologous to the dunce learning and memory
 A:Reference number: A54442; MUID:94019330
 A:Accession: 161354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-736 <RES>
 A:Cross-references: GB:L20966; NID:g347121; PIDN:AAA03589.1; PID:g347122
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
 F:405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 736;
 Best Local Similarity 31.3%; Pred. No. 5e-37;
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

QY 66 KKKVKKRLS-----FQRYFHASRLRLGIIIPQAPRLHLDLDEYLGQARHMLSKVGMDFDEL 121
 126 KKKQOQMTQISGVKKLMHSSLNNTSISRGVNTENDHAKLEEDLNK--WGLNIFN 182
 QY 122 FDRLTNGNSLVTLCHLFNTHGLIHFKLDVTLHRLVWQEDYHSQNPYHNAVHADV 181
 183 VAGSHNRPLICIMYALFOERDILKTRISSDTFTYMTLEDHYHSAVAHNSLHADV 242
 QY 182 TOAHNCYKLEPKLASFLPLDLMGLAAAHADVHGVPNPFLIKTNHNLANTYONKSV 241
 243 AOSTHVLSTPALDAVFTDEILIAIFAAIHVDHGVSNQFLINTSELTALMYNDESV 302
 QY 242 LENHNRSTIGMLRESR--LLAHLPKEMTODIEOGLSLATDINRQNEFLTRKALH 299
 303 LENHNLAVGFKLQDEHODIFMNLTKKQROQLRKMYIDVMTATMSKMSLLADKTWE 362
 QY 300 NKD-----LRLDAORHFMLOIALKADICNCRITWEMSKSERVECFYRQGELEQ 353
 363 TKKVTSSGVLLDDVYTRIGVLRMMVHCADLSNPTKSLEYRQWTDRIEMEFPOQDGER 422
 QY 354 KFELEISPLCNOQKDSIPISQIGFMSYIVPELPFEMAHFTGNSTLSENMLGHLANKAOW 413
 423 ERGMEISPMCDKHTASVEKSGVGFIDYIVHPLMETWADLVOPD--AQDILDTLEDNRMY 480
 QY 414 KSLPLRQHRSGSGSGP-----DHDHAG-----QGTSEEQEED 448
 481 QSMTPQ-----SPSPPLDEQNRDCQGLMEKFOFELTLDEDESGPERKEGE 525

RESULT 10
 161354
 C:Species: Homo sapiens (man)
 C:Date: 26-Jul-1996 #sequence.revision 26-Jul-1996 #text_change 21-Jul-2000
 C:Accession: A54442; S55788; A56317; S55787
 R:Boiger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M.; Cell. Biol. 13, 6558-6571, 1993
 A:Title: A family of human phosphodiesterases homologous to the dunce learning and memory
 A:Reference number: A54442; MUID:94019330
 A:Accession: A54442
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-886 <RES>
 A:Cross-references: GB:L20965; NID:g347119; PIDN:AAA03588.1; PID:g347120
 R:Sullivan, M.; Egerton, M.; Shakur, Y.; Marguardsen, A.; Houslay, M.D.
 A:Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of
 A:Reference number: S55788; MUID:95194817
 A:Accession: S55788
 A:Molecule type: mRNA
 A:Residues: 'MCPPTVTV', 210-735, 'E', 737-886 <SUT>
 A:Cross-references: EMBL:U18087; NID:9604374; PIDN:AA050458.1; PID:9604375
 A:Note: 736-Ala was also found
 R:Li, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Mol. Cell. Biol. 10, 2678-2686, 1990
 A:Title: Cloning and expression of cDNA for a human low-K⁺ m, rolipram-sensitive cycl
 A:Reference number: A36317; MUID:90258854
 A:Accession: A36317
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'MCPPTVTV', 210-516, 'Y', 518-722, 'R', 724-726, 'R', 728-735, 'E', 737-788, 'E',
 A:Cross-references: GB:M37744
 C:Genetics:
 A:Gene: GDB:PDE4A, DPDE2
 A:Cross-references: GDB:138776; OMIM:600126
 A:Map position: 19p13.1-19q12
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
 C:Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
 F:432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.5%; Score 565; DB 2; Length 886;

Best Local Similarity 32.1%; Pred. No. 1e-36;
Matches 126; Conservative 82; Mismatches 165; Indels 20; Gaps 6;

```

OY 69 VKRLSFQRYFHASRLRRIIPQAPRLHLDDEYLGQARHMSKQGMDFIDFLDRLNG 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 332 MSQITGLKLMHNSNLSNINIPRGVKTQDELLAQLLENLNK---WGILNFCVSDYAG 388
OY 129 NSLVTLCHLFNTGHIHNFKIDMTLHREFLVMQEDHSONPKNHNAVDVQAMHCY 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 RSLTCIMYMIPOERDLKKFERIPVDVTYMTLLEDDHADVAYHNSLHADVLOSHVL 448
OY 189 LKPEKIASFLTPRLDITGLAAADVDHDPGVNOFLKKTNNHLANLQNNASYLENHWR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 449 LARPDAVETDELELAFMAAIIHDVDPGVSNQFLINTNSLALMYNDESYLENHHLA 508
OY 249 STIGMLRESR--LNAHPKEMTODIEOOLGSLIATDINRONFLTRKALHNKD---- 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 509 VGKLLQEDNCDIFQNLRSKROSLRKAVIDKVLATDSKMTLLADLKTWVEETKVTSS 568
OY 303 --LRLEADQDRHFMQIALKCADICNPKRIMSKQSEKCEERYRQGELEQKFELEIS 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 569 GVLIDNYSDRIOVLNNVHCADLSNPTRKLELYRQMTDRMAFFPOQDREKRGMEIS 628
OY 361 PLCNQOKDSIPSIQIFMSYIEPLRFEMAHFTGNSTLSENMGLAHNKAQMSKL--- 417
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 629 PMCKRTASVEKSOVGFIIDYIVHPMETWADLVHPD--AOEILDLEDDNRWYSALROS 686
OY 418 ---PROHRSRSGSG-PDHDHAGOGTESEGE 446
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 687 PSPPREESRGCHRPDPKQFELLLEEEBE 719

RESULT 11
167946
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N:Alternate names: cyclic AMP-specific phosphodiesterase RDL; RHPDD41
M:Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Aug-2001
C:Accession: 167946; A32558; B32558; C32558
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A>Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A:Reference number: 153865; MUID:95047482
A:Accession: 167946
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: GB:L27062; NID:g436013; PIDN:AAA56859.1; PID:g436014
R:Davis, R.L.; Takayasu, H.; Eberly, M.; Myers, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A>Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+) g
A:Reference number: A32558; MUID:8264472
A:Accession: A32558
A:Molecule type: mRNA
A:Residues: 1-598, 'T', 600-610 <DAV>
A:Cross-references: GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:g203983; GB:J04554
A:Molecule type: mRNA
A:Residues: 85-120, 154-598, 'T', 600-610 <DA2>
A:Cross-references: GB:M26716; GB:J04554; NID:g203986; PIDN:AAA41102.1; PID:g
A>Note: Splice form RD2
A:Accession: C32558
A:Molecule type: mRNA
A:Residues: 26-598, 'T', 600-610 <DA3>
A:Cross-references: GB:M26716; NID:g203984; PIDN:AAA41101.1; PID:g203985; GB:J04554
A>Note: Splice form RD3
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F:14-20/Region: responsible for membrane association
F:26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pr
F:85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #s

```

F:184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.2%; Score 559.5; DB 2; Length 610;
Best Local Similarity 31.1%; Pred. No. 1.7e-36;
Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;

```

OY 43 RGSYPIDFRLNSTTSGEIGTKKKVRLSPQRYFHASRLRIGIIPQAPRLHLDDEY 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 RQSQMSQITGLKLVHNGSLTN-----VPRGVKTQDEDL 117
OY 103 GQARHMSKVGWMDPFLPRLTNGSLVTLCHLFNTGHIHNFKIDMTLHREFLVMY 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 AQELENLK---WGILNFCVSEYAGRSLSCIMVTIQRDLKKFHPVDMMYMTL 174
OY 163 QEDYSONPYHNAVAADVQAMHCYIKPEKIASFLTPRLDITGLAAADVDHDPGVN 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 EDHYHADVAHNSLHADVLOSHVLTARPDAVETDELELAFMAAIIHDVDPGVSN 234
OY 223 PELKTNNHLANLYONMSYLENNHWRSTIGMLRSR--LNAHPKEMTODIEOOLGSL 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 QFLINTNSLALMYNDESYLENHHLAVGFKLLQEDNCDIFQNLRSKROSLRKAVIDMVL 294
OY 281 AFDINRQNEFLTRKALHNKD-----LRLEADQDRHFMQIALKCADICNPKRIMES 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 ATDMSKHMTLADLKTWVEETKVTSSGVLIDNYSDRIOVLNNVHCADLSNPTRKLEY 354
OY 335 KQMSERVCSEERYRQGELEISPLCNQOKDSIPSIQIFMSYIEPLRFEMAHFTG 394
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 355 RQMTDRMAFFPOQDREKRGMEISPMCKDHTASVEKSOVGFIIDYIVHPMETWADLVH 414
OY 395 NSTLSENMGLAHNKAQMSKLPRQHRSRSGSGP-DHDHAGOG-----TE 441
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 PD-AODILDLEDDNR-DW-----YHSAIROSPSPLEERPGIGHPSPDKFOFELT 465
OY 442 SEQEGDS 449
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 466 EEEEEEDS 473

RESULT 12
153865
phosphodiesterase - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Sep-2000
C:Accession: 153865
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A>Title: Differential CNS expression of alternative mRNA isoforms of the mammalian ge
A:Reference number: 153865; MUID:95047482
A:Accession: 153865
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-844 <RES>
A:Cross-references: GB:L27057; NID:g3334904; PIDN:AAC27098.1; PID:g436004
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F:418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

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Query Match 23.2%; Score 559.5; DB 2; Length 844;
Best Local Similarity 31.1%; Pred. No. 2.6e-36;
Matches 133; Conservative 77; Mismatches 163; Indels 55; Gaps 9;

```

OY 43 RGSYPIDFRLNSTTSGEIGTKKKVRLSPQRYFHASRLRIGIIPQAPRLHLDDEY 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 RQSQMSQITGLKLVHNGSLTN-----VPRGVKTQDEDL 351
OY 103 GQARHMSKVGWMDPFLPRLTNGSLVTLCHLFNTGHIHNFKIDMTLHREFLVMY 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 AQELENLK---WGILNFCVSEYAGRSLSCIMVTIQRDLKKFHPVDMMYMTL 408
OY 163 QEDYSONPYHNAVAADVQAMHCYIKPEKIASFLTPRLDITGLAAADVDHDPGVN 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 409 EDHYHADVAHNSLHAADVLQSTHVLATPALDVAFTDLELALFAAAIHVDHPGVSN 468
 QY 223 PELIKTHHNLANTYONNSVLENNHWRSTIGMLRESR--LLAHLPRKEMTODIEOGLSLIL 280
 Db 469 QFLINTSEILAMNDNSVLENNHVLAVGFKLQENCDIPONLSKRORSRKRVADIMVL 528
 QY 281 ATDINRONEFLTRKKAHLHNKD-----LRLDAODRHFMLOIALKCADICNPCRIMEMS 334
 Db 529 ATMSKMTLADLKTWVERKVTSSGVLLDNDYSDRIQYLRNVHCADLSNPTKPELY 588
 QY 335 KONSERCEEFYRQGELEOKFELEISPLCNOQKDSIPSIQIGMSYIVERPLFREMAHFTG 394
 Db 589 RQMTDRIMAEFFQGDREEREGEISPMCDKHTASVEKSGVGFIDYIVHPLMETWADLVH 648
 QY 395 NSTLSEMMGLHANKAKQWKSLLPROHRSRGSSGSP-DHDHMGQ-----TE 441
 Db 649 PD--AQDILDTLEDNR-DW-----YHAIROSFSPLEEPGGLGHPSLDPKQFELTL 699
 QY 442 SEBOEGDS 449
 Db 700 EEEBESDS 707

RESULT 13

S71626
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human
 N:Alternate names: 3',5'-cyclic AMP phosphodiesterase
 C:Species: Homo sapiens (man)
 C>Date: 27-Nov-1997 #sequence,revision 12-Dec-1997 #text_change 17-Nov-2000
 C:Accession: S71626; I61356
 R:Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.
 FEBS Lett. 358, 305-310, 1995
 A>Title: Molecular cloning and functional expression in yeast of a human cAMP-specific P
 A:Reference number: S71626; MUID:95145731
 A:Accession: S71626
 A:Molecule type: DNA
 A:Residues: 1-712 <ENG>
 A:Cross-references: EMBL:Z46632; NID:9727222; PIDN:CAA86601.1; PID:9727223
 A:Experimental source: substantia nigra
 R:Boiger, G.; Michael, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
 Moll. Cell. Biol. 13, 6558-6571, 1993
 A>Title: A family of human phosphodiesterases homologous to the dunce learning and mem
 A:Reference number: A54442; MUID:94019330
 A:Accession: I61356
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 462-712 <RES>
 A:Cross-references: GB:L20968; NID:9347125; PIDN:AAA03591.1; PID:9347126
 C:Genetics:
 A:Gene: HSPDEAC1
 C:Function:
 A:Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP
 A:Pathway: cyclic nucleotide metabolism
 A:Note: expressed in various tissues but not in cells of the immune system
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
 C:Keywords: phosphoric diester hydrolase
 F:387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.0%; Score 553; DB 2; Length 712;
 Best Local Similarity 27.8%; Pred. No. 6.8e-36;
 Matches 135; Conservative 94; Mismatches 198; Indels 58; Gaps 10;

QY 11 ELIFENDQNAKCYCMGLRIGQTVRAERRCSTPFIDFRLLN-----STTYG-- 61
 Db 204 KLALETLDLWDCLDQLETQTRHSVGEASNKR-----RLNRELTLHSETSRSGNQ 257
 QY 62 -----EIGTKR-----KVRLSPQRYPHASRLGLIIPQAPLHLDE 99
 Db 258 VSEYISTFTDQTEVLELPKVTAEAPQPMRSRISGLGLCHSASLSATYPRFVQTDQE 317
 QY 100 DYLGQAHHMLSKVGMDFDIFLEDRLTNGNSLVTLCHLEFNTGGLIHFKLDMVTLHRL 159

Db 318 EQLAKE---LEDITKMGLDVEFKVADVSGNRPETAIIFESIFQERDLTKFOIPADTLATYL 374
 QY 160 VMQEDHSONPRYNANVAHADVYQAMHCYLKEPRLASFRLPDMGLLAAADVDYHPG 219
 Db 375 LMEGHYHANVAHNSLHAADVASTHVLATPLAEVFDLETLALFSAIHVDYHPG 434
 QY 220 VNQFLIKTHHNLANTYONNSVLENNHWRSTIGMLRESR--LLAHLPRKEMTODIEOGLS 277
 Db 435 VSNQFLINTSDVALAMNDNSVLENNHVLAVGFKLQENCDIPONLSAKORLSIRRAVID 494
 QY 278 LILATDINRONEFLTRKKAHLHNKD-----LRLDAODRHFMLOIALKCADICNPCRIM 331
 Db 495 MVLATDSKHMNLADLKTWVERKVTSSGVLLDNDYSDRIQYLRNVHCADLSNPTKPL 554
 QY 332 EMSKSERCEEFYRQGELEOKFELEISPLCNOQKDSIPSIQIGMSYIVERPLFREMAH 391
 Db 555 PLRWQMTDRIMAEFFQGDREEREGEISPMCDKHTASVEKSGVGFIDYIVHPLMETWAD 614
 QY 392 FTGNSTLSEMMGLHANKAKQWKSLLPROHRS-RGSSGSGPDH-----DHAGQTESE 443
 Db 615 LVHFD--AQDILDTLEDNRKREYQSKIPRSBDLTNPERDGPDRQFELTLFEAEEDDEE 672
 QY 444 EQEGD 448
 Db 673 EEEGE 677

RESULT 14

I67945
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)
 N:Alternate names: cAMP phosphodiesterase 1
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 29-May-1998 #sequence,revision 29-May-1998 #text_change 03-Nov-2000
 C:Accession: I67945; A33904
 R:Boiger, G.B.; Rodgers, L.K.; Riggs, M.
 Gene 149, 237-244, 1994
 A>Title: Differential CNS expression of alternative mRNA isoforms of the mammalian g
 A:Reference number: I53865; MUID:95047482
 A:Accession: I67945
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-536 <RES>
 A:Cross-references: GB:L27061; NID:9436011; PIDN:AAA56858.1; PID:9436012
 R:Swinnen, J.V.; Joseph, D.R.; Conti, M.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
 A>Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce ca
 A:Reference number: A33904; MUID:89315790
 A:Accession: A33904
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 230-496 <SWT>
 A:Cross-references: GB:M25347; GB:M28410
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
 C:Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
 F:253-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 22.0%; Score 529.5; DB 2; Length 536;
 Best Local Similarity 30.8%; Pred. No. 3.4e-34;
 Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;

QY 71 RLISFORFYHNASRLRGITPOAPRLHLDEVLGQARIMLSKVGWMDIFLEDRLTNGNS 130
 Db 156 QITGLRKSCHTS-LPTAIPRFVGYQTQDEELAKE---LEDITKMGLDVFKVAELSGNRP 211
 QY 131 LVTLCHLFTNTHGLIHFKLDMVTLARFLVWVQEDYHSONPRYNANVAHADVYQAMHCYLK 190
 Db 212 LTAVTFPVLQERDLTKFOIPADTLRLYLTLLEGHYSNVAHNSHAADVYQSAHYLLG 271
 QY 191 EPKLASFLLPDMIGLAAAHADVDHPRGVNQRPRLTITNHHNLANTYONNSVLENNHWRST 250
 Db 272 TPALAEAVFTDLEVLAAIFACAIHVDHDPGVSNQFLINTNSLALMYNDSSVLENNHVLAVG 331

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OY      251  IGMJRSR--LLAHJPKMTODIFOOGLSIIITDINQNEPFLTYKXHLHNKO-----302
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      332  FKJLQENGDIFQNSTQKSLRRWIMDVNLATDMSKMSLLADLKMTYETKVSIGV 351
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      303  LRJEDODHFMJLALACADICPCIKWMSQNSEERCEEFYQOGLQKFELEISPL 362
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      392  ILLDNTSDRIQVLSLVHACADLSNPAKPLRYIOMYTERMAEFEPQOGRSESLDISPM 451
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      363  CNOQKDSIPISIOIGMSTIYEPFLREMAHFTGNTSLSENMGLAHNKAQKSLPLRQHR 422
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      452  CQDHNTASVKSQVGTIDIAIPLMEWADLVHPD--AQELDTLEDNREMYQSRVP-----505
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      423  SRSGSGSGPDH---DHAGQGTSESEEDCD 448
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      506  CSDPNAIGDPRKFELEETFEETFEEDDE 534
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 15

hypothetical protein R153.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
C:Accession: T16769
R:Kirsten, J
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid R153.
A:Reference number: Z18573
A:Accession: T16769
A:Status: preliminary; translated from GR/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1549 <R>
A:Cross-references: EMBL:U28729; NID:9861238; PTD:9861239; PIDN:AAA68292.1; CESP:R153.1
A:Experimental source: strain Bristol N2
A:Genetics:
A:Gene: CESP.R153.1
A:Initons: 23/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3
A:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match	21.5%	Score 517:	DB 2:	Length 549:
Best Local Similarity	32.6%	Pred. No. 3,56-33:		
Matches 114:	Conservative 72:	Mismatches 140:	Indels 24:	Gaps 6:
QY	105	ARHMLSYGMMDDIDELPRLTNGNSLVTLLCHLNTNTGLLNHNRKLDMTVLHRELYVMQD	164	
DB	216	AVHM-QRLDDMGDPVKIDELSKNSHSLVYVTSLRQRNKRKTEIHQSTLYLLNLNE	274	
QY	165	DYHSQNYHNHNAAYTQAMHCYKEKPKLASFLPLDIMGILLAAADVDHPGYNQDP	224	
DB	275	HYRN-NHYHNFTHAADVAOSMHALMSPLVLEVFDEIVLALTAAGVAVHVDHPTGTNOY	333	
QY	225	LKTNHHLAALYQMSYLENNHNRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLLAT	282	
DB	334	LINSNELALMYDESVLEQDHHLAFAFKLQDSNCDFLANSTRQRLOFKRIYIDVLTAL	393	
QY	283	DINRQNEFLTRLKALH-----NRDLRLDAQDRHFMLQITALKACADICNPPCRIMWSKO	336	
DB	394	DMSHEMSLADLKTMYEAKKVGANNVYIDLYKDKIKTQVLOSIMHLDLNPTRPIELYOQ	453	
QY	337	WSEVFCEEFYRQGELEQKFELEISPLCNQOKDIPSIDIGMSYATPLPRREVAHNTGNS	396	
DB	454	WNOIIMEYVRODQDKREKLEGTLEISPMCRGNVYITEKSOVGFIDIVYPLRETVADLVYPD	513	
QY	397	TLEENMIGHLAHHKAAQMSKSLPRQHSRGSQSGSDPHDHGQOGSESEQD	446	
DB	514	-KONITDQLEENREYVQSRIP-----EDPTATVYDEDEHK	549	